

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 54.5455 Seconds  
(without alignments)  
125.735 Million cell updates/sec

Title: US-10-758-165a-1  
Perfect score: 81  
Sequence: 1 RNDSPQTQDTQYTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	81	100.0	15	ADR10601	Adr10601 Dog Ige e
2	81	100.0	312	AAV79995	Aav79995 Dog immun
3	81	100.0	417	AAW23067	Aaw23067 Canine Ig
4	81	100.0	426	AAW97753	Aaw97753 Canine Ig
5	81	100.0	426	ABP96583	Abp96583 Dog Ige h
6	53	65.4	15	ADR10607	Adr10607 Pig Ige e
7	53	65.4	567	ABP96588	Abp96588 Pig Ige h
8	48	59.3	15	ADR10602	Adr10602 Cat Ige e
9	48	59.3	431	ADG73237	Adg73237 Cat immun
10	48	59.3	496	ABP96580	Abp96580 Cat Ige h
11	48	59.3	496	ABU09338	Abu09338 Feline Ig
12	48	59.3	496	ABU09336	Abu09336 Feline Ig
13	48	59.3	496	ADG73251	Adg73251 Cat parti
14	48	59.3	496	ADG73225	Adg73225 Cat parti
15	43	53.1	1633	ABU42513	Abu42513 Proteine
16	42	51.9	1067	ABB91309	Abb91309 Herbicida
17	41	50.6	15	ADR10603	Adr10603 Horse Ige
18	41	50.6	151	AAU57418	Aau57418 Propionib
19	41	50.6	151	ARM53937	Arm53937 Propionib
20	41	50.6	424	AAW50103	Aaw50103 Equine Ig
21	41	50.6	424	AAW50104	Aaw50104 Equine Ig
22	41	50.6	533	ABP39208	Abp39208 Staphyloc
23	41	50.6	533	ADS05754	Ads05754 Staphyloc

24	41	50.6	566	9	AED15438	Aed15438 Equine Pr
25	41	50.6	566	10	AE888000	Aee88000 Human pro
26	41	50.6	569	6	ABP96585	Abp96585 Horse Ige
27	40	49.4	356	4	ABB64299	Abb64299 Drosophil
28	40	49.4	488	8	ADY09532	Ady09532 Plant ful
29	40	49.4	555	6	ADA24243	Ada24243 Pseudomon
30	40	49.4	632	7	ABM90457	Abm90457 Rice abio
31	40	49.4	632	7	ABM85909	Abm85909 Rice abio
32	40	49.4	659	10	AER24334	Aer24334 Esterase
33	40	49.4	667	6	ADA33007	Ada33007 Acinetoba
34	40	49.4	1180	3	AAB01845	Aab01845 Haemophil
35	40	49.4	1188	3	AAB01844	Aab01844 Haemophil
36	40	49.4	2349	6	AAO16359	Aao16359 Human tra
37	40	49.4	2400	4	ABG20278	Abg20278 Novel hum
38	40	49.4	2415	4	ABG20279	Abg20279 Novel hum
39	39	48.1	226	8	ADRA4996	Adra4996 SnsAG3 an
40	39	48.1	276	3	AAG08697	Aag08697 Arabidops
41	39	48.1	276	3	AAG42639	Aag42639 Arabidops
42	39	48.1	281	8	ADI28921	Adi28921 Sarcocyst
43	39	48.1	281	8	ADR44989	Adr44989 Sarcocyst
44	39	48.1	294	3	AAG08696	Aag08696 Arabidops
45	39	48.1	294	3	AAG42638	Aag42638 Arabidops

ALIGNMENTS

RESULT 1  
ADRI0601  
ID ADR10601 standard; peptide; 15 AA.  
XX ADR10601;  
XX  
DT 21-OCT-2004 (first entry)  
DE Dog Ige epitope recognised by monoclonal antibody 5.91, SEQ ID 1.  
XX  
KW Antiaethmatic; Antiallergic; Immunosuppressive; Ige; dog; asthma;  
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
OS Canis familiaris.  
XX  
PN W02004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
(UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
DR WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian Ige epitope, useful  
PT for testing an allergen reactivity of Ige sample, detecting mammalian Ige  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian Ige epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige.  
CC (I) is useful for testing an allergen reactivity of an Ige sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian Ige and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine Ige corresponding to amino acid  
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
CC canine Ige epsilon-chain. Recognition of epsilon-chains from Ige from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15  
 |||||  
 Db 1 RNDSPQTQDQYTTTG 15

## RESULT 2

AAW79995  
 ID AAW79995 standard; protein; 312 AA.

XX AC AAW79995;

XX XX 15-MAY-2000 (first entry)

XX DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-aesthetic; asthma; anaphylaxis; dermatitis.

XX OS Canis sp.

XX PN WO9967293-A1.

XX XX 29-DEC-1999.

XX XX 21-JUN-1999; 99WO-US013959.

XX XX 20-JUN-1998; 98US-00100287.

XX XX (UNBI-) UNITED BIOMEDICAL INC.

XX XX Wang CV, Walfield AM;

XX DR WPI; 2000-160578/14.

XX XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

XX XX Example 1; Page 66-68; 155pp; English.

XX XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAW79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 312 AA;

Query Match 100.0%; Score 81; DB 3; Length 312;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RNDSPQTQDQYTTTG 15  
 |||||  
 Db 255 RNDSPQTQDQYTTTG 269

## RESULT 3

AAW23067  
 ID AAW23067 standard; protein; 417 AA.

XX AC AAW23067;

XX XX 30-JUN-2005 (revised)

XX DT 16-JUN-2005 (revised)

XX DT 19-FEB-1998 (first entry)

XX DE Canine IgE heavy chain constant region (exon 1-4 product).

XX KW IgE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX OS Canis familiaris.

XX XX Key Location/Qualifiers

FT FT Misc-difference 55 /note= "encoded by ACC"

FT FT Misc-difference 56 /note= "encoded by TAC"

FT FT Misc-difference 67 /note= "encoded by GCC"

FT FT Misc-difference 83 /note= "encoded by NNT"

FT FT Misc-difference 174 /note= "encoded by GGN"

FT FT Misc-difference 175 /note= "encoded by NNG"

FT FT Misc-difference 176 /note= "encoded by TGN"

FT FT Misc-difference 203 /note= "encoded by TCC"

FT FT Misc-difference 204 /note= "encoded by GAC"

XX XX WO9730156-A2.

XX XX 21-AUG-1997.

XX XX 14-FEB-1997; 97WO-US002322.

XX XX 14-FEB-1996; 96US-00601197.

XX XX (IDEX-) IDEXX LAB INC.

XX XX Mermer B, Harris RA, Siefring AE;

XX XX WPI; 1997-425031/39.

XX XX N-PSDB; AAT79278.

XX XX Isolated canine IgE heavy chain constant region DNA - useful to develop  
 PT products for treatment of canine allergies and for immunomodulation in  
 PT dogs.

XX XX Disclosure; Page 35-39; 59pp; English.

XX XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE  
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat Type I immediate hypersensitivity, and for immunomodulation

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CC Revised record issued on 30-JUN-2005 : Typo in comments
XX
SQ Sequence 417 AA;

Query Match      100.0%; Score 81; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
Db 352 RNDSPQTQDQYTTTG 366

RESULT 4
AAR97753
ID AAR97753 standard; protein; 426 AA.
XX
AC AAR97753;
XX
DT 28-AUG-1996 (first entry)
XX
DE Canine IgE.
XX
KW IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX
OS Canis familiaris.
XX
PN WO9614867-A1.
XX
XX
XX 23-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US013795.
XX
PR 09-NOV-1994; 94US-00336583.
XX
PR 09-NOV-1994; 94US-00336891.
XX
PA (NERI ) MERCK & CO INC.
XX
XX Hollis GF, Patel MD;
XX
DR WPI; 1996-277321/28.
DR N-PSDB; AAT29824.
XX
XX New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX
XX Claim 11; Page 29-30; 49pp; English.
XX
XX The canine IgE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAT29824) obtd. from a canine liver DNA library. The
CC cloning of the IgE gene allows prodn. of large quantities of recombinant
CC IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IgE antibody generation). Fragments of IgE can be
CC used in vaccines or to prevent IgE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IgE-mediated immune
XX responses
XX
SQ Sequence 426 AA;

Query Match      100.0%; Score 81; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
Db 357 RNDSPQTQDQYTTTG 371

RESULT 5
ABP96583
ID ABP96583 standard; protein; 426 AA.

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XX ABP96583;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dog IgE heavy chain amino acid sequence SEQ ID NO:28.
XX
KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
KW immune response; major histocompatibility complex; MHC; immunogenic;
KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KW urticaria hives.
XX
XX Canis familiaris.
OS
XX WO2003015716-A2.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 08-AUG-2002; 2002WO-US026986.
PF
XX
XX 13-AUG-2001; 2001US-0312120P.
PR
XX
XX (IGET-) IGE THERAPEUTICS INC.
PA
XX
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX
XX WPI; 2003-268242/26.
DR
XX
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IgE, by identifying peptide eliciting CTL response to IgE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
XX Example 7; Page 152-154; 187pp; English.
XX
XX The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IgE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IgE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IgE, and in
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IgE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
SQ Sequence 426 AA;

Query Match      100.0%; Score 81; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
Db 357 RNDSPQTQDQYTTTG 371

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AC ADR10602;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.  
 XX  
 KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KW cat.  
 XX  
 XX  
 OS Felis catus.  
 XX  
 PN W02004065936-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 XX 15-JAN-2004; 2004WO-US003566.  
 PF  
 PR 16-JAN-2003; 2003US-0440472P.  
 XX  
 PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hammerberg B;  
 XX  
 XX WPI; 2004-593545/57.  
 DR  
 XX  
 XX Novel antibody that specifically binds to mammalian IgE epitope, useful  
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 PT or treating asthma or anaphylactic shock.  
 XX  
 XX Example 6; Page 9; 14pp; English.  
 XX  
 XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IgE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC cat IgE 5.91 recognition site.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 59.3%; Score 48; DB 8; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 0.33;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 NDSPIQTDQYTTT 14  
 ||||:|:|  
 Db 2 NDSFVRTEQQATT 14  
 ||||:|:|  
 RESULT 9  
 ADG73237  
 ID ADG73237 standard; protein; 431 AA.  
 XX  
 AC ADG73237;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Cat immunoglobulin E (IgE) constant region.  
 XX  
 KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;  
 KW immune response; IgE-mediated response; allergy; cat; constant region.  
 XX

OS Felis catus.  
 XX  
 PN US2003216565-A1.  
 XX  
 PD 20-NOV-2003.  
 XX  
 XX 07-APR-2003; 2003US-00409772.  
 PF  
 XX 07-JAN-1999; 99US-0115033P.  
 PR  
 PR 07-JAN-2000; 2000US-00479614.  
 XX  
 XX (MCCA/) MCCAII C.  
 PA (WEBE/) WEBER E..  
 XX  
 XX McCall C, Weber E;  
 PI  
 XX WPI; 2004-010802/O1.  
 DR  
 DR N-PSDB; ADG73236.  
 XX  
 XX New isolated nucleic acid molecule encoding a portion of a feline IgE  
 PT heavy chain protein, useful for treating and/or eliciting feline immune  
 PT responses for IgE-mediated responses, such as allergies.  
 XX  
 XX Claim 12; SEQ ID NO 14; 44pp; English.  
 XX  
 XX The invention describes an isolated nucleic acid molecule (I) encoding a  
 CC portion of a feline IgE heavy chain protein. The methods and compositions  
 CC of the present invention are useful for eliciting feline immune responses  
 CC for and/or treating IgE-mediated responses, such as allergies. This is  
 CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.  
 XX  
 XX SQ Sequence 431 AA;  
 Query Match 59.3%; Score 48; DB 8; Length 431;  
 Best Local Similarity 61.5%; Pred. No. 12;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 NDSPIQTDQYTTT 14  
 ||||:|:|  
 Db 363 NDSFVRTEQQATT 375  
 ||||:|:|  
 RESULT 10  
 ABP96580  
 ID ABP96580 standard; protein; 496 AA.  
 XX  
 AC ABP96580;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Cat IgE heavy chain amino acid sequence SEQ ID NO:25.  
 XX  
 XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
 KW immune response; major histocompatibility complex; MHC; immunogenic;  
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.  
 XX  
 OS Felis catus.  
 XX  
 PN W02003015716-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 XX 08-AUG-2002; 2002WO-US026986.  
 PF  
 PR 13-AUG-2001; 2001US-0312120P.  
 XX  
 XX (IGET-) IGE THERAPEUTICS INC.  
 PA  
 XX Chen SA, Yang Y, Barankiewicz T, Chen 2;  
 PI

XX WPI; 2003-268242/26.  
 XX  
 DR Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 XX against IgE, by identifying peptide eliciting CTL response to IgE  
 PT peptides naturally presented by major histocompatibility complex class I  
 PT protein.  
 XX  
 XX Example 7; Page 145-147; 187pp; English.  
 PS  
 XX The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IGE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IGE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,  
 CC vasotropic, dermatological, anti-inflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in  
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an IGE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention  
 XX  
 SQ Sequence 496 AA;

Query Match 59.3%; Score 48; DB 6; Length 496;  
 Best Local Similarity 61.5%; Pred. No. 14;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
 ||||:|:| ||  
 Db 428 NDSFVRTEQQATT 440

RESULT 11  
 ABU09338  
 ID ABU09338 standard; protein; 496 AA.

XX AC ABU09338;

XX DT 27-JUN-2003 (first entry)

XX DE Feline IGE epsilon heavy chain #2.

XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
 KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
 KW antibody technology; antiallergic; antiparasitic; cytostatic.

XX OS Felis catus.

XX FN US2003013183-A1.

XX PD 16-JAN-2003.

XX PF 07-JAN-2000; 2000US-00479614.

XX PR 07-JAN-1999; 99US-0115033P.

XX PA (MCCA/) MCCALL C.  
 XX PA (WEBE/) WEBER E.

XX PI

PI McCall C, Weber E;  
 XX  
 DR WPI; 2003-391997/37.  
 DR N-PSDB; ABX95715.  
 XX  
 PT New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or  
 PT light chain protein, useful for treating feline IGE-mediated responses  
 PT e.g. allergies, parasitic infections or neoplasia.  
 XX  
 XX Claim 1; Page 37-39; 45pp; English.  
 PS  
 XX The present invention relates to the isolation of feline immunoglobulin E  
 CC (IgE) kappa light chain and IGE epsilon heavy chain proteins, and the  
 CC polynucleotide sequences encoding them. The sequences of the invention  
 CC are useful for treating feline IGE-mediated immune responses (e.g.  
 CC allergies, parasitic infections or neoplasia), in vaccine technology,  
 CC small molecule/antibody technology, molecular biology, and various  
 CC immunological techniques related to feline IGE and its functions. The  
 CC present sequence represents feline IGE epsilon heavy chain #2  
 XX  
 SQ Sequence 496 AA;  
 Query Match 59.3%; Score 48; DB 6; Length 496;  
 Best Local Similarity 61.5%; Pred. No. 14;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
 ||||:|:| ||  
 Db 428 NDSFVRTEQQATT 440

RESULT 12  
 ABU09336  
 ID ABU09336 standard; protein; 496 AA.

XX AC ABU09336;

XX DT 27-JUN-2003 (first entry)

XX DE Feline IGE epsilon heavy chain #1.

XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
 KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
 KW antibody technology; antiallergic; antiparasitic; cytostatic.

XX OS Felis catus.

XX FH Key Location/Qualifiers  
 XX Region 66.496  
 XX /note= "This sequence is given as SEQ ID No.14 and is  
 XX specifically claimed in Claim 12"  
 XX Region 284.309  
 XX /note= "This sequence is given as SEQ ID No.11 and is  
 XX specifically claimed in Claim 9"  
 XX Region 288.305  
 XX /note= "This sequence is given as SEQ ID No.8 and is  
 XX specifically claimed in Claim 10"  
 XX Region 291.302  
 XX /note= "This sequence is given as SEQ ID No.5 and is  
 XX specifically claimed in Claim 11"

XX FN US2003013183-A1.

XX PD 16-JAN-2003.

XX PF 07-JAN-2000; 2000US-00479614.

XX PR 07-JAN-1999; 99US-0115033P.

XX PA (MCCA/) MCCALL C.  
 XX PA (WEBE/) WEBER E.

XX PI McCall C, Weber E;

```
XX WPI; 2003-391997/37.
DR N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
XX Claim 1; Page 24-25; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #1
XX
XX Sequence 496 AA;
SQ
Query Match 59.3%; Score 48; DB 6; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 NDSPIQTDQYTTT 14
Db 428 NDSFVRTEQQATT 440
RESULT 13
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
AC ADG73251;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat partial immunoglobulin E (IgE) heavy chain #2.
XX
XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
XX immune response; IgE-mediated response; allergy; cat; heavy chain.
XX
XX Felis catus.
XX
XX US2003216565-A1.
XX
XX 20-NOV-2003.
XX
XX 07-APR-2003; 2003US-00409772.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX (MCCA/) MCCALL C.
XX (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2004-010802/01.
XX N-PSDB; ADG73250.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IgE
XX heavy chain protein, useful for treating and/or eliciting feline immune
XX responses for IgE-mediated responses, such as allergies.
XX
XX Claim 8; SEQ ID NO 29; 44pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX portion of a feline IgE heavy chain protein. The methods and compositions
XX of the present invention are useful for eliciting feline immune responses
XX for and/or treating IgE-mediated responses, such as allergies. This is
XX the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
XX chain.
XX
XX Sequence 496 AA;
SQ
Query Match 59.3%; Score 48; DB 8; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 NDSPIQTDQYTTT 14
Db 428 NDSFVRTEQQATT 440
RESULT 15
ABU42513
ID ABU42513 standard; protein; 1633 AA.
XX
```

AC ABU42513;  
XX 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #28040.  
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Staphylococcus epidermidis.  
XX WO200277183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
FA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
PI WPI; 2003-029926/02.  
XX N-PSDB; ACA46383.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 70437; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 1633 AA;

Query Match 53.1%; Score 43; DB 6; Length 1633;  
Best Local Similarity 61.5%; Pred. No. 3.7e+02;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14  
Db 242 NDEFTQDVEYTTT 254

Search completed: August 30, 2006, 04:22:07  
Job time : 55.5455 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 8.93939 Seconds  
(without alignments)  
161.448 Million cell updates/sec

Title: US-10-758-165a-1

Perfect score: 81

Sequence: 1 RNDSPITQDQYTTTG 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80.\*

2: pir1.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	53.1	664	2 T20420	hypothetical prote
2	42	51.9	1008	2 T32986	hypothetical prote
3	42	51.9	1067	2 D96545	probable DNA polym
4	41	50.6	1117	2 S63399	probable membrane
5	40	49.4	1234	2 T49737	hypothetical prote
6	40	49.4	1157	2 F97255	fusion of alpha-gl
7	40	49.4	2094	2 S33124	tpi protein - huma
8	39	48.1	187	2 JC4806	core protein G - p
9	39	48.1	187	2 S22331	gene G protein - p
10	39	48.1	294	2 T08408	transcription fact
11	39	48.1	514	2 S72443	DNA-binding protei
12	39	48.1	564	1 HMIVDA	hemagglutinin prec
13	39	48.1	587	2 F85084	probable athila-li
14	39	48.1	940	2 T01834	hypothetical prote
15	39	48.1	2161	1 A45389	genome polyprotein
16	39	48.1	26926	1 T38344	titin, cardiac mus
17	38.5	47.5	1157	1 S49247	parasporeal crystal
18	38	46.9	173	2 S55150	hypothetical prote
19	38	46.9	201	2 T31492	hypothetical prote
20	38	46.9	205	2 T31489	hypothetical prote
21	38	46.9	254	2 F81265	cysQ protein homol
22	38	46.9	281	2 AD2052	hypothetical prote
23	38	46.9	321	2 B32801	fimbrial adhesin p
24	38	46.9	335	2 JE0115	zinc-finger protei
25	38	46.9	429	2 E84410	GTP-binding protei
26	38	46.9	450	2 A10345	probable heat choc
27	38	46.9	468	2 T08139	shaggy-like protei
28	38	46.9	612	2 C90374	hypothetical prote
29	38	46.9	996	2 S76194	hypothetical prote

30	38	46.9	1158	2 AF1852	hypothetical prote
31	38	46.9	1450	2 A44027	165K myofibrillar
32	38	46.9	1465	2 S43529	165K protein, skel
33	38	46.9	1562	2 T07323	DNA-directed RNA p
34	38	46.9	1969	2 T38495	hypothetical prote
35	37.5	46.3	272	2 B69688	glutamate racemase
36	37.5	46.3	590	2 S63193	hypothetical prote
37	37	45.7	136	2 F84234	hypothetical prote
38	37	45.7	219	2 E71841	hypothetical prote
39	37	45.7	245	2 T23844	hypothetical prote
40	37	45.7	268	2 A71966	hypothetical prote
41	37	45.7	298	2 A70238	hypothetical prote
42	37	45.7	429	2 T06296	extensin-like prot
43	37	45.7	502	2 E71963	probable cardiolip
44	37	45.7	521	2 A48650	agrocarnopine utili
45	37	45.7	521	2 A13244	hypothetical prote

ALIGNMENTS

RESULT 1

T20420

hypothetical protein E02H4.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T20420

R;Barlow, K.

submitted to the EMBL Data Library, November 1995

A;Reference number: Z19273

A;Accession: T20420

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-664 <WIL>

A;Cross-references: UNIPROT:Q19038; UNIPARC:UPI0000129186; EMBL:Z68003; PIDN:CAA91975.1;

A;Experimental source: clone E02H4

C;Genetics:

A;Gene: CESP:E02H4.1

A;Map position: X

A;Introns: 57/3; 102/3; 135/3; 166/1; 191/1; 221/2; 254/3; 314/2; 355/2; 386/1; 472/3; 5

C;Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe

Query Match 53.1%; Score 43; DB 2; Length 664;

Best Local Similarity 80.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIOTDQYTTT 14

| | | | |

Db 536 PCQDQYTTT 545

RESULT 2

T32986

hypothetical protein C05D2.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C;Accession: T32986

R;Du, Z.

submitted to the EMBL Data Library, February 1998

A;Description: The sequence of C. elegans cosmid C05D2.

A;Reference number: Z21260

A;Accession: T32986

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-1008 <DUZ>

A;Cross-references: UNIPARC:UPI000017B734; EMBL:AF047651; PIDN:AA02723.1; GSPDB:GN00021

A;Experimental source: strain Bristol N2; clone C05D2

C;Genetics:

A;Gene: CESP:C05D2.6

A;Map position: 3

A;Introns: 23/1; 53/3; 141/1; 231/3; 307/3; 325/2; 420/1; 466/3; 499/3; 522/2; 594/1; 75

Query Match 51.9%; Score 42; DB 2; Length 1008;

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Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPIQTDQYT 12
   |||:|:|
Db 41 REDPPVKTQYT 52

RESULT 3
D96545
probable DNA polymerase A family protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D96545
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1067 <STO>
A;Cross-references: UNIPROT:Q9C6J5; UNIPARC:UPI0000048370; GB:AE005173; NID:gl1094700; F
C;Genetics:
A;Gene: F8A12.8
A;Map position: 1

Query Match 51.9%; Score 42; DB 2; Length 1067;
Best Local Similarity 42.9%; Pred. No. 41;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTG 15
   |||:|:|
Db 625 SDSPLSTNFATSG 638

RESULT 4
S63399
probable membrane protein YNR067c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N3547
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63399
R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Accession: S63399
A;Molecule type: DNA
A;Residues: 1-1117 <DUE>
A;Cross-references: UNIPROT:P53753; UNIPARC:UPI000013BACB; EMBL:271682; NID:gl302597; PI
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNR067c
A;Cross-references: SGD:S0005350
A;Map position: 14R
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>

Query Match 50.6%; Score 41; DB 2; Length 1117;
Best Local Similarity 58.3%; Pred. No. 65;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTT 13
   |||:|:|
Db 430 NDGPITQNKFT 441
```

```
RESULT 5
T49737
hypothetical protein B24B19.90 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49737
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <SCH>
A;Cross-references: UNIPARC:UPI0000179D8A; EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.90
A;Experimental source: BAC clone B24B19; strain OR74A
C;Genetics:
A;Gene: NCSP:B24B19.90
A;Map position: 6
A;Introns: 132/2
C;Superfamily: Neurospora crassa hypothetical protein B24B19.90

Query Match 49.4%; Score 40; DB 2; Length 234;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTDQYTTT 14
   |||:|:|
Db 65 PVPTQYTTT 74

RESULT 6
F97255
fusion of alpha-glucosidase (family 31 glycosyl hydrolase) and glycosidase (Trea/Mals fa
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97255
R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:121359325
A;Accession: F97255
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1157 <KUR>
A;Cross-references: UNIPROT:Q97F62; UNIPARC:UPI00000D755C; GB:AE001437; PIDN:AAK80833.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2891

Query Match 49.4%; Score 40; DB 2; Length 1157;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTT 13
   |||:|:|
Db 889 NESDVFTEQYTT 900

RESULT 7
S33124
tpr protein - human
N;Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S33124; S23740; S00928; G01185
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
A;Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive coi
A;Reference number: S33124; MUID:93064711; PMID:1437155
A;Accession: S33124
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Molecule type: mRNA  
A;Residues: 1-2094 <MIT>  
A;Cross-references: UNIPROT:Q15624; UNIPROT:Q9UE33; UNIPARC:UPI000017CBF3; EMBL:X66397;  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
R;Mitchell, P.J.; Cooper, C.S.  
Oncogene 7, 383-388, 1992  
A;Title: Nucleotide sequence analysis of human tpr cDNA clones.  
A;Reference number: S23740; MUID:52195670; PMID:1549355  
A;Accession: S23740  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-725, 'L', <MI2>  
A;Cross-references: UNIPARC:UPI0000062253; EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID  
R;King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.  
Oncogene 2, 617-619, 1988  
A;Title: Tpr homologues activate met and raf.  
A;Reference number: S00928; MUID:88262257; PMID:3387099  
A;Accession: S00928  
A;Molecule type: mRNA  
A;Residues: 1-31, 'R', 33-142 <KIN>  
A;Cross-references: UNIPARC:UPI000016B112; EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID  
R;Greco, A.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: H00592  
A;Accession: G01185  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 144-228 <GRE>  
A;Cross-references: UNIPARC:UPI00000711D7; EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; F  
C;Genetics:  
A;Gene: GDB:TPR  
A;Cross-references: GDB:128821; OMIM:189940  
A;Map position: 1q25-1q25  
A;Introns: 177/3

Query Match 49.4%; Score 40; DB 2; Length 2094;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 5 PIQTDQVTTT 14  
DB 1922 PLQSDQQT 1931  
RESULT 8  
JC4806  
core protein G - phage phi-K  
C;Species: phage phi-K  
C;Date: 15-Aug-1996 #sequence\_revision 15-Oct-1996 #text\_change 09-Jul-2004  
C;Accession: JC4806; B04253; A04253  
R;Kodaira, K.; Oki, M.; Kakikawa, M.; Kimoto, H.; Taketo, A.  
J. Biochem. 119, 1062-1069, 1996  
A;Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant ph  
A;Reference number: JC4804; MUID:96424987; PMID:8827438  
A;Accession: JC4806  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-187 <KOD>  
A;Cross-references: UNIPROT:Q38042; UNIPARC:UPI0000138658; EMBL:X60323; NID:g1478118; PI  
R;Sims, J.; Capon, D.; Dressler, D.  
J. Biol. Chem. 254, 12615-12628, 1979  
A;Title: dnaG (primase)-dependent origins of DNA replication. Nucleotide sequences of th  
A;Reference number: A92247; MUID:80049950; PMID:387790  
A;Accession: B04253  
A;Molecule type: DNA  
A;Residues: 165-187 <SIM>  
A;Cross-references: UNIPARC:UPI000009C0FB  
C;Comment: This protein is one of the structural components of the bacteriophage capsid.  
C;Genetics:  
A;Gene: G  
C;Superfamily: phage phi-X174 gene G protein  
C;Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;  
Best Local Similarity 40.0%; Pred. No. 19;  
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
QY 1 RNDSPITQTDQVTTTG 15  
DB 8 KHDTAIQTSRFSVTG 22  
RESULT 9  
S22331  
gene G protein - phage alpha-3  
C;Species: phage alpha-3  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C;Accession: S22331; C04253; A04253  
R;Kodaira, K.I.; Nakano, K.; Okada, S.; Taketo, A.  
Biochim. Biophys. Acta 1130, 277-288, 1992  
A;Title: Nucleotide sequence of the genome of the bacteriophage alpha3: interrelationshi  
A;Reference number: S22324; MUID:92223109; PMID:1532908  
A;Accession: S22331  
A;Molecule type: DNA  
A;Residues: 1-187 <KOD>  
A;Cross-references: UNIPROT:P31281; UNIPARC:UPI0000113352; EMBL:X60322; NID:g14775; PIDN  
R;Sims, J.; Capon, D.; Dressler, D.  
J. Biol. Chem. 254, 12615-12628, 1979  
A;Title: dnaG (primase)-dependent origins of DNA replication. Nucleotide sequences of th  
A;Reference number: A92247; MUID:80049950; PMID:387790  
A;Accession: C04253  
A;Molecule type: DNA  
A;Residues: 165-187 <SIM>  
A;Cross-references: UNIPARC:UPI0000000389; GB:J02444; GB:M10725; NID:g166103; PIDN:AAA32  
C;Comment: This protein is one of the structural components of the bacteriophage capsid.  
C;Genetics:  
A;Gene: G  
C;Superfamily: phage phi-X174 gene G protein  
C;Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;  
Best Local Similarity 40.0%; Pred. No. 19;  
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
QY 1 RNDSPITQTDQVTTTG 15  
DB 8 KHDTAIQTSRFSVTG 22  
RESULT 10  
T08408  
transcription factor homolog F18B3.150 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T08408  
R;Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub  
submitted to the Protein Sequence Database, May 1999  
A;Reference number: Z16409  
A;Accession: T08408  
A;Molecule type: DNA  
A;Residues: 1-294 <QUE>  
A;Cross-references: UNIPROT:Q9SVL2; UNIPARC:UPI000000A322F; EMBL:AL049862; GSPDB:GNO00061;  
A;Experimental source: cultivar Columbia; BAC clone F18B3  
C;Genetics:  
A;Gene: ATSP:F18B3.150  
A;Map position: 3  
A;Introns: 172/3

Query Match 48.1%; Score 39; DB 2; Length 294;  
Best Local Similarity 75.0%; Pred. No. 33;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 4 SPIQTDQY 11  
DB 201 APVQTDQY 208

## RESULT 11

S72443  
DNA-binding protein WRKY1 - parsley  
C;Species: Petroselinum crispum (parsley)  
C;Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 31-Dec-2004  
C;Accession: S72443  
R;Rushton, P.J.; Tovar Torres, J.; Parniske, M.; Wernart, P.; Hahlbrock, K.; Somasich, I.  
EMBO J. 15, 5690-5700, 1996  
A;Title: Interaction of elicitor-induced DNA-binding proteins with elicitor response element  
A;Reference number: S72443; MUID:97051827; PMID:8896462  
A;Molecule type: mRNA  
A;Residues: 1-514 <RUS>  
A;Cross-references: UNIPROT:Q40827; UNIPARC:UPI000000A1PF5; EMBL:U48831; NID:gl431871; PID:  
C;Superfamily: DNA-binding protein WRKY1  
C;Keywords: DNA binding

Query Match 48.1%; Score 39; DB 2; Length 514;  
Best Local Similarity 70.0%; Pred. No. 61;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSPIQTDQYTT 12  
|:|||||:  
Db 53 DSPIQNNYTT 62

## RESULT 12

HM1VDA  
hemagglutinin precursor - influenza A virus  
N;Contains: hemagglutinin HA1; hemagglutinin HA2  
C;Species: influenza A virus  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 16-Jun-2000  
C;Accession: B39987; A04057; F33157  
R;Nobusawa, E.; Aoyama, T.; Kato, H.; Suzuki, Y.; Tateno, Y.; Nakajima, K.  
Virology 182, 475-485, 1991  
A;Title: Comparison of complete amino acid sequences and receptor-binding properties among  
A;Reference number: A39987; MUID:91220697; PMID:2024485  
A;Accession: B39987  
A;Molecule type: genomic RNA  
A;Residues: 1-564 <NOB>  
A;Cross-references: UNIPARC:UPI000012C4D8; GB:D90307; NID:g221309; PIDN:BAA14337.1; PID:  
A;Experimental source: strain A/duck/Alberta/60/76 [H12N5]  
R;Ait, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7639-7643, 1981

A;Title: Sequence relationships among the hemagglutinin genes of 12 subtypes of influenza  
A;Reference number: A39902; MUID:82150925; PMID:6174976  
A;Accession: A04057  
A;Molecule type: genomic RNA  
A;Residues: 1-38, L',40-51, G',53-101 <AIR>  
A;Cross-references: UNIPARC:UPI0000170F31; GB:J02104; NID:g324135; PIDN:AAA43180.1; PID:  
A;Experimental source: strain A/duck/Alberta/60/76 [H12]  
A;Note: the signal sequence and the amino end of the HA1 chain comprise residues 1-17 and  
C;Genetics:

A;Map position: segment 4  
C;Superfamily: influenza virus hemagglutinin  
C;Keywords: glycoprotein; hemagglutinin; homotrimer; transmembrane protein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-342/Product: hemagglutinin HA1 #status predicted <HA1>  
F;343-564/Product: hemagglutinin HA2 #status predicted <HA2>  
F;535-551/Domain: transmembrane #status predicted <TM1>  
F;27,28,140,151,152,222,302,309,496,523/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 48.1%; Score 39; DB 1; Length 564;  
Best Local Similarity 60.0%; Pred. No. 68;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTDQYTTT 14  
|:|||||:  
Db 174 PVQTDYKNT 183

## RESULT 13

A;Cross-references: UNIPROT:P24658; UNIPARC:UPI0000172721; GB:L13195; NID:g289531; PID:g

## F85084

probable athila-like protein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: F85084  
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; MUID:20083488; PMID:10617198  
A;Accession: F85084  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-587 <STO>  
A;Cross-references: UNIPROT:Q9W0T2; UNIPARC:UPI000009E989; GB:NC\_001268; NID:g7267490; P:  
C;Genetics:

A;Gene: At4g08490  
A;Map position: 4

Query Match 48.1%; Score 39; DB 2; Length 587;  
Best Local Similarity 66.7%; Pred. No. 71;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DSPIQTDQYTTT 14  
|:|||||:  
Db 401 DTPPQTDQNPPT 412

## RESULT 14

T01834  
hypothetical protein T15F16.4 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: T01834  
R;Antoniou, B.; Lee, T.  
submitted to the EMBL Data Library, August 1998  
A;Description: The sequence of A. thaliana T15F16.  
A;Reference number: Z14443  
A;Accession: T01834  
A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: DNA  
A;Residues: 1-940 <ANT>  
A;Cross-references: UNIPROT:O81471; UNIPARC:UPI000009DA3B; EMBL:AF076275; NID:g3293582;  
A;Experimental source: cultivar Columbia  
C;Genetics:

A;Map position: 4  
A;Introns: 108/1; 340/1  
A;Note: T15F16.4

Query Match 48.1%; Score 39; DB 2; Length 940;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DSPIQTDQYTTT 14  
|:|||||:  
Db 754 DTPPQTDQNPPT 765

## RESULT 15

A45389  
genome polyprotein - canine distemper virus (strain Onderstepoort)  
N;Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase  
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)  
C;Species: canine distemper virus  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: A45389  
R;Sidhu, M.S.; Menonna, J.P.; Cook, S.D.; Dowling, P.C.; Udem, S.A.  
Virology 193, 50-65, 1993  
A;Title: Canine distemper virus L gene: sequence and comparison with related viruses.  
A;Reference number: A45389; MUID:93174968; PMID:8438585

A;Accession: A45389  
A;Molecule type: genomic RNA  
A;Residues: 1-2161 <SID>  
A;Cross-references: UNIPROT:P24658; UNIPARC:UPI0000172721; GB:L13195; NID:g289531; PID:g



C;Genetics:  
A;Gene: L  
C;Superfamily: parainfluenza virus RNA-directed RNA polymerase  
C;Keywords: Atp; nucleotidyltransferase; RNA biosynthesis; RNA replication  
Query Match 48.1%; Score 39; DB 1; Length 2161;  
Best Local Similarity 63.6%; Pred. No. 3.1e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 NDSPIQTDQYT 12  
|||  
Db 1656 NDKFILDQYS 1666

Search completed: August 30, 2006, 04:30:58  
Job time : 9.93939 secs

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 58.4848 Seconds  
(without alignments)  
237.245 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPQTQDTTGTG 15

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	59.3	196	2	Q3KZ66 SCHJA
2	46	56.8	363	2	Q2SB97 9GAMM
3	45	55.6	585	2	Q47P11 THEFY
4	44	54.3	558	2	Q6FJW7 CANGA
5	43.5	53.7	515	2	Q3SN12 NITWN
6	43	53.1	310	2	Q3DWS5 CHLAU
7	43	53.1	340	2	Q4SKB2 TETNG
8	43	53.1	511	2	Q5HK05 STAEQ
9	43	53.1	511	2	Q8CMU2 STAES
10	43	53.1	516	2	Q7RHP3 PLAYO
11	43	53.1	634	2	Q2VB08 9BACT
12	43	53.1	664	1	DEL1 CAEEL
13	43	53.1	699	2	Q819P8 9BIVA
14	43	53.1	809	2	Q4N289 THEPA
15	43	53.1	5261	2	Q4UFT9 THEAN
16	42	51.9	127	2	Q3PUR9 NITHA
17	42	51.9	273	2	Q5WK1 NEUCR
18	42	51.9	392	2	Q3MYA8 9DEL1
19	42	51.9	455	2	Q2XAG3 PSEPU
20	42	51.9	455	2	Q88D16 PSEPK
21	42	51.9	459	2	Q3KIR7 PSEPF
22	42	51.9	515	2	Q400L8 CAEEL
23	42	51.9	516	2	Q45133 CAEEL
24	42	51.9	700	2	Q24781 BACSP
25	42	51.9	1049	2	Q9W105 ARATH
26	42	51.9	1067	2	Q9C6J5 ARATH
27	42	51.9	1857	2	Q8TW75 METAC
28	41	50.6	189	2	Q87R22 VIBPA
29	41	50.6	235	2	Q4L7X7 STAHU
30	41	50.6	264	2	Q4MVN6 BACCE
31	41	50.6	299	2	Q6CIY1 KLUFA

32	41	50.6	339	2	Q8RBP9 THETN	Q8rbp9 thermoanaer
33	41	50.6	360	2	Q8A5I8 BACTN	Q8A5I8 bacteroides
34	41	50.6	414	2	Q5TRD3 ANOGA	Q5trd3 anopheles g
35	41	50.6	429	2	Q757X1 ASHGO	Q757x1 ashbya goss
36	41	50.6	662	2	Q6FN92 CANGA	Q6fn92 candida gla
37	41	50.6	713	2	Q5QV82 IDILO	Q5qv82 idiomarina
38	41	50.6	860	2	Q6JWS3 9BACT	Q6jws3 uncultured
39	41	50.6	1117	1	ENGL YEAST	P53753 saccharomyc
40	40	49.4	97	2	Q3RS02 RALME	Q3rs02 raistonia m
41	40	49.4	99	2	Q60S88 CABER	Q60s88 caenorhabdi
42	40	49.4	213	2	Q5WCK0 BACSK	Q5wck0 bacillus cl
43	40	49.4	234	2	Q7RUA3 NEUCR	Q7rua3 neurospora
44	40	49.4	236	2	Q56PA2 9METZ	Q56pa2 uncultured
45	40	49.4	255	2	Q54Z36 DICDI	Q54z36 dictyostei

ALIGNMENTS

RESULT 1  
Q3KZ66 SCHJA  
ID Q3KZ66 SCHJA PRELIMINARY; PRT; 196 AA.  
AC Q3KZ66;  
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.  
DT 08-NOV-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE SICHG06457 protein (Fragment).  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatoidea; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,  
RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,  
RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Peng Z., Chen Z.,  
RA Han Z.-G.;  
RT "New Perspectives on Host-parasite Interplay by Comparative  
RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,  
RT Schistosoma japonicum."  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL; AY809222; ABA40295.1; -; mRNA.  
DR NON TER 196 196  
FT NON TER 196 196  
SQ SEQUENCE 196 AA; 21675 MW; C04EF1B36AFFAA87 CRC64;  
Query Match 59.3%; Score 48; DB 2; Length 196;  
Best Local Similarity 57.1%; Pred. No. 5.4;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 NDSPIQTQDTTGTG 15  
Db 131 SNSPVTQYETTGTG 144  
RESULT 2  
Q2SB97 9GAMM  
ID Q2SB97 9GAMM PRELIMINARY; PRT; 363 AA.  
AC Q2SB97;  
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.  
DT 24-JAN-2006, sequence version 1.  
DT 07-FEB-2006, entry version 2.  
DE DNA repair photolyase.  
GN ORFNames=HCH 05408;  
OS Habella chejuensis KCTC 2396.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;  
OC Habellaceae; Habella.  
OX NCBI\_TaxID=349521;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=KCTC 2396;
RX PubMed=16352867; DOI=10.1093/nar/gki1016;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
RT "Genomic blueprint of Haella chejuensis, a marine microbe producing
RL an algicidal agent";
RL Nucleic Acids Res. 33:7066-7073 (2005).
CC -----
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CC -----
DR EMBL: CP000155; ABC32077.1; -; Genomic_DNA.
KW GO: GO:0016829; F:lyase activity; IEA.
SQ SEQUENCE 363 AA; 41267 MW; 8A2619C94CC8D185 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 363;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTG 15
Db 339 RRDSPRLRLDLPFG 353

RESULT 3
Q47PF1 THEFY
ID Q47PF1 THEFY PRELIMINARY; PRT; 585 AA.
AC Q47PF1
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE Putative solute-binding dependent transport lipoprotein precursor.
GN OrderedLocusNames=Tfu_1633;
OS Thermobifida fusca (strain YX).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptosporangineae; Nocardiopsaceae; Thermobifida.
OX NCBI_TaxID=269800;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Di Bartolo G., Chain P., Schmutz J.,
RA Larimer F., Land M., Lykidis A., Richardson P.;
RT "Complete sequence of Thermobifida fusca YX."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: CP000088; AA255668.1; -; Genomic_DNA.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00496; SEP_bac_5; 1.
DR PRINTS: PR01415; ANKYRIN.
KW Complete proteome; Lipoprotein; Signal.
FT SIGNAL 1 31 Potential.
SQ SEQUENCE 585 AA; 64409 MW; E4E1PFC382E87931 CRC64;

Query Match 55.6%; Score 45; DB 2; Length 585;
Best Local Similarity 64.3%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSPHTDVIETG 15
Db 381 NDSPHTDVIETG 394

RESULT 4
Q6FW7_CANGA
ID Q6FW7_CANGA PRELIMINARY; PRT; 558 AA.

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AC Q6FW7;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 18.
DE Candida glabrata strain CBS138 chromosome M complete sequence.
GN OrderedLocusNames=CAGL0M0303g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E., Barbe V.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Bleykasten C.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -----
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CC -----
DR EMBL: CR380959; CAG62453.1; -; Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR007114; MFS.
DR InterPro: IPR011701; MFS_1.
DR Pfam: PF07690; MFS_1; 1.
DR PROSITE: PS00850; MFS; 1.
KW Complete proteome; Membrane; Transmembrane; Transport.
SQ SEQUENCE 558 AA; 61177 MW; 05760736C3F432D CRC64;

Query Match 54.3%; Score 44; DB 2; Length 558;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSPQTQDQYTTG 15
Db 69 NDSPQNPVEYFETG 82

RESULT 5
Q3SN12_NITWN
ID Q3SN12_NITWN PRELIMINARY; PRT; 515 AA.
AC Q3SN12;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocusNames=Nwi_3082; ORFNames=Nwi_3082;
OS Nitrobacter winogradskyi (strain NB-255 / ATCC 25391).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Nitrobacter.
OX NCBI_TaxID=323098;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,

```

RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,  
 RA Vargel L., Schmutz J., Larimer F., Land M., Hauser L., Kyriades N.,  
 RA Lykidis A., Richardson P.;  
 RT "Complete sequence of *Nitrobacter winogradskyi* NB-255.";  
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.  
 CC  
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 CC  
 CC EMBL; CP000115; ABA06329.1; -; Genomic DNA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0008170; F:N-methyltransferase activity; IEA.  
 DR GO; GO:0006306; P:DNA methylation; IEA.  
 DR InterPro; IPR002296; N12N6\_mfrase.  
 DR InterPro; IPR002052; N6\_Mcase.  
 DR PRINTS; PR00507; N12N6MTFRASE.  
 DR PROSITE; PS00092; N6\_MTASE; UNKNOWN 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 515 AA; 54223 MW; 4F973B39D823B669 CRC64;  
 Query Match 53.7%; Score 43.5; DB 2; Length 515;  
 Best Local Similarity 60.0%; Pred. No. 1e+02;  
 Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 RNDSPQTQDQYTTTG 15  
 DB 420 RNDAPVLTD-YDTVG 433  
 RESULT 6  
 Q3DW55 CHLAU  
 ID Q3DW55 CHLAU PRELIMINARY; PRT; 310 AA.  
 AC Q3DW55;  
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.  
 DT 22-NOV-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Peptidase C60, sortase A and B.  
 GN ORFNames=CaurDRAFT\_1873;  
 OS *Chloroflexus aurantiacus* J-10-fl.  
 OC Bacteria; Chloroflexi; Chloroflexales; Chloroflexaceae; Chloroflexus.  
 OX NCBI\_TaxID=324602;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=J-10-fl;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
 RA Hammon N., Israni S., Pitluck S., Richardson P.;  
 RT "Sequencing of the draft genome and assembly of *Chloroflexus*  
 RT *aurantiacus* J-10-fl.";  
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=J-10-fl;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer P., Land M.;  
 RT "Annotation of the draft genome assembly of *Chloroflexus aurantiacus*  
 RT J-10-fl.";  
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=J-10-fl;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
 RA Hammon N., Israni S., Pitluck S., Richardson P.;  
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

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 CC  
 CC EMBL; AAAH02000045; EAO57904.1; -; Genomic DNA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0009058; P:biosynthesis; IEA.  
 SQ SEQUENCE 310 AA; 33946 MW; EDB84C3A584E6B7 CRC64;  
 Query Match 53.1%; Score 43; DB 2; Length 310;  
 Best Local Similarity 53.3%; Pred. No. 70;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 RNDSPQTQDQYTTTG 15  
 DB 61 RGDSPLPAPQLTSG 75  
 RESULT 7  
 Q4SKB2 TETNG  
 ID Q4SKB2 TETNG PRELIMINARY; PRT; 340 AA.  
 AC Q4SKB2;  
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Chromosome 13 SCAF14566, whole genome shotgun sequence.  
 GN ORFNames=GSTENG00016807001;  
 OS *Tetradontoides* (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15496914; DOI=10.1038/nature03025;  
 RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;  
 RT "Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC  
 CC EMBL; CAAE01014566; CAF98920.1; -; Genomic DNA.  
 SQ SEQUENCE 340 AA; 36745 MW; 1E282568C07674E5 CRC64;  
 Query Match 53.1%; Score 43; DB 2; Length 340;  
 Best Local Similarity 53.3%; Pred. No. 78;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 RNDSPQTQDQYTTTG 15  
 DB 322 RLDAPLADQNATG 336

```

RESULT 8
ID QSHKQ5_STAEQ PRELIMINARY; PRT; 511 AA.
AC QSHKQ5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE 5'-nucleotide family protein.
GN OrderedLocusNames=SERP2289;
OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=176279;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uitterback T.R., Lee C.,
RA Dmitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RT J. Bacteriol. 187:2426-2438(2005).
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EMBL; CP000029; AAW53170.1; -; Genomic_DNA.
DR TIGR; SERP2288; -
GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0000166; P:nucleotide binding; IEA.
GO; GO:0009166; P:nucleotide catabolism; IEA.
InterPro; IPR008334; 5'-Nucleotidase C.
InterPro; IPR006146; 5'-Nucleotidase N.
InterPro; IPR006179; 5'-Nucleotidase.
InterPro; IPR004843; M-pesterase.
PANTHER; PTHR11575; 5_nucleotidase; 1.
Pfam; PF02872; 5_nucleotid_C; 1.
PRINTS; PR01607; APYRASEFAMLY.
PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
Complete proteome; Metal-binding; Nucleotide-binding.
KW Staphylococcus epidermidis strain.
SQ SEQUENCE 511 AA; 5798 MW; 5798 MW; 47487BE2096ADEC6 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTT 13
DB 444 NDAPIQSDQIYT 455
|||||:|
|:|:|:|

RESULT 10
Q7RHP3_PLAYO PRELIMINARY; PRT; 516 AA.
AC Q7RHP3;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE GAF domain protein.
GN ORfNames=PY03941;
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=17XNU;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kool J.T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
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CC -----
DR EMBL; AABL01001174; EAA15729.1; -; Genomic_DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Complete proteome; Lyase.
SQ SEQUENCE 516 AA; 62120 MW; 8CBA858FA3C373FC CRC64;

Query Match 53.1%; Score 43; DB 2; Length 516;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPIDTDOY 11
Db :|||:||||
53 KNDEPVSTDRY 63

RESULT 11
Q2VBUS_9BACT Q2VBUS_9BACT PRELIMINARY; PRT; 634 AA.
AC Q2VBUS_9BACT
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE RTX toxins and related Ca2+-binding protein (Fragment).
OS uncultured Bacteroidetes bacterium 'SB12-18 P41A3'.
OC Bacteria; Bacteroidetes; environmental samples.
OX NCBI_TaxID=358068;
RN [1]
RA COTTRELL M.T., YU L., KIRCHMAN D.L.;
RP "Sequence and Expression Analyses of Cytophaga-Like Hydrolases in a
RT Western Arctic Metagenomic Library and the Sargasso Sea.";
RL Appl. Environ. Microbiol. 71:8506-8513(2006).
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CC -----
DR EMBL; DQ272742; AB886523.1; -; Genomic_DNA.
DR NON TER 634
SQ SEQUENCE 634 AA; 66581 MW; 339F60245E3B994B CRC64;

Query Match 53.1%; Score 43; DB 2; Length 634;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db :|||:||||
498 NDAPIDTQSVST 510

RESULT 12
DEL1_CABEL DEL1_CABEL STANDARD; PRT; 664 AA.
AC Q19036;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 21-FEB-2006, entry version 39.
DE Degenerin del-1.
GN Name=del-1; ORFNames=E02H4.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Bristol N2;
RA Tavernarakis N., Shreffler W., Wang S.L., Driscoll M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for

investigating biology.";
Science 282:2012-2018(1998).
-|- FUNCTION: Probable sodium channel subunit.
-|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
-|- SIMILARITY: Belongs to the amiloride-sensitive sodium channel
family.
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EMBL; U76403; AAB39735.1; -; mRNA.
EMBL; Z68003; CAA91975.1; -; Genomic_DNA.
PIR; T20420; T20420.
DR Ensembl; E02H4.1; Caenorhabditis elegans.
DR WormBase; WBGene0000952; del-1.
DR WormPep; E02H4.1; CE05547.
DR InterPro; IPR004726; Deg-1.
DR InterPro; IPR001873; Na+channel_ASC.
DR PANTHER; PTHR11690; Na+channel_ASC; 1.
DR Pfam; PF00858; ASC; 1.
DR PRINTS; PR01078; AMINACHANNEL.
DR TIGRFAMs; TIGR00867; deg-1; 1.
DR PROSITE; PS01206; ASC; 1.
KW Complete proteome; Glycoprotein; Ion transport; Ionic channel;
KW Membrane; Sodium; Sodium channel; Sodium transport; Transmembrane;
KW Transport.
FT CHAIN 1 664 Degenerin del-1.
FT /FTID=PRO_0000181285.
FT TOPO_DOM 1 67 Cytoplasmic (Potential).
FT TRANSMEM 68 88 Potential.
FT TOPO_DOM 89 607 Extracellular (Potential).
FT TRANSMEM 608 628 Potential.
FT TOPO_DOM 629 664 Cytoplasmic (Potential).
FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 394 394 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 508 508 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 562 562 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 664 AA; 75474 MW; 0D19C8EF7968F8D CRC64;

Query Match 53.1%; Score 43; DB 1; Length 664;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
Db :|||:||||
536 PCQDQYTTT 545

RESULT 13
Q819P8_9BIVA Q819P8_9BIVA PRELIMINARY; PRT; 699 AA.
AC Q819P8;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 2.
DT 07-FEB-2006, entry version 16.
DE Alpha-amylase.
GN Name=AmY;
OS Corbicula fluminea.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Corbiculoidea; Corbiculidae; Corbicula.
OX NCBI_TaxID=45949;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Da Lage J.-L., Van Wormhoudt A., Cariou M.-L.;
RT "Diversity and evolution of the alpha-amylase genes in Animals.";
RL Biologia 57:181-189(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14704857; DOI=10.1007/s00018-003-3334-y;
RA Da Lage J.-L., Feller G., Jansek S.;
RT "Horizontal gene transfer from Eukarya to bacteria and domain
shuffling: the alpha-amylase model.";
RT
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RL Cell. Mol. Life Sci. 61:97-109(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Da Lage J.-L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC -----
DR EMBL; AF468016; AA017927.2; -; Genomic_DNA.
DR HGSP; P04745; 1SMD.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR InterPro; IPR006048; Alpha_ami1_C.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1_13.
DR Pfam; PF02806; Alpha-amylase; 1_2.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C; 1.
SQ SEQUENCE 699 AA; 76544 MW; 25D57008165B04CB CRC64;

Query Match 53.1%; Score 43; DB 2; Length 699;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPQIOTDQYTTTG 15
Db 241 QSNPEIKTSQTSIG 255

RESULT 14
Q4N289 THEPA
ID Q4N289 THEPA PRELIMINARY; PRT; 809 AA.
AC Q4N289
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=TP04_0468;
OS Theileria parva;
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OC NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA Crabtree J., Wortman J.R., Haas B., Anguoli S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Utterback T.R., Feldblyum T.V., Fertea M.,
RA Allen J., Nierman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Anguoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Fertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;

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RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AKG01000004; EAN31820.1; -; Genomic_DNA.
DR Hypothetical protein.
SQ SEQUENCE 809 AA; 92620 MW; 58FA8368C3613471 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 809;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 NDSPIOTDQYTTTG 15
Db 526 NNSPTSNSSEPTTG 539

RESULT 15
Q4UFT9 THEAN
ID Q4UFT9 THEAN PRELIMINARY; PRT; 5261 AA.
AC Q4UFT9
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 03-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Sfil-subtelomeric related protein family member, putative.
GN ORFNames=TA16050;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OC NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RX PubMed=15994597; DOI=10.1258/jrsm.98.7.320;
RA Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,
RA Kerhornou A., Aletti M., Bishop R., Bouchier C., Cochet M.,
RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Fosker N.,
RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
RA Larke N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
RA Nene V., O'Neil S., Price C., Quail M.A., Rabinowitsch E.,
RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
RA Langsley G., Rajandream M.-A., McKeever D., Shiels B., Tait A.,
RA Barrell B., Hall N.;
RT "Genome of the host-cell transforming parasite Theileria annulata
RT compared with T. parva.";
RL Science 309:131-133(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
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CC -----
DR EMBL; CR940348; CAI74027.1; -; Genomic_DNA.
DR InterPro; IPR013320; ConA_like_subgrp.
DR Pfam; PF04385; FAINT; 54.
DR Kinase; Repeat; Transferase.
SQ SEQUENCE 5261 AA; 603934 MW; 79941BB6659B78E CRC64;

Query Match 53.1%; Score 43; DB 2; Length 5261;
Best Local Similarity 53.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIOTDQYTTT 14
Db 4887 NDNPETKNDYTTT 4899

Search completed: August 30, 2006, 04:29:24
Job time : 61.4848 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 14.8485 Seconds  
(without alignments)  
88.424 Million cell updates/sec

Title: US-10-758-165a-1

Perfect score: 81

Sequence: 1 RNDSPQTQDQYTTTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs,\* 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	108	2	US-09-281-760E-37
2	81	100.0	312	2	US-09-701-623C-2
3	81	100.0	426	1	US-08-336-583-2
4	81	100.0	426	5	PCT-US95-13795-2
5	48	59.3	431	2	US-09-479-614-14
6	48	59.3	496	2	US-09-479-614-2
7	48	59.3	496	2	US-09-479-614-29
8	41	50.6	533	2	US-09-134-001C-4053
9	40	49.4	163	2	US-09-270-767-43446
10	40	49.4	667	2	US-09-328-352-4294
11	40	49.4	1180	2	US-09-206-942-65
12	40	49.4	1180	2	US-10-193-764-61
13	40	49.4	1188	2	US-09-206-942-63
14	40	49.4	1188	2	US-10-193-764-59
15	40	49.4	2186	2	US-09-949-016-10828
16	40	49.4	2349	2	US-09-538-092-914
17	38.5	47.5	625	1	US-08-532-547-7
18	38.5	47.5	625	1	US-08-532-547-9
19	38.5	47.5	625	2	US-09-019-809-7
20	38.5	47.5	625	2	US-09-019-809-9
21	38.5	47.5	625	2	US-09-471-177-7
22	38.5	47.5	625	2	US-09-471-177-9
23	38.5	47.5	1156	2	US-09-002-285-72
24	38.5	47.5	1156	2	US-09-589-477-72
25	38.5	47.5	1156	2	US-09-661-322A-28
26	38.5	47.5	1156	2	US-10-099-285A-72

27 38.5 47.5 1157 1 US-08-532-547-5 Sequence 5, Appli  
28 38.5 47.5 1157 1 US-08-379-656B-5 Sequence 5, Appli  
29 38.5 47.5 1157 2 US-08-455-838-5 Sequence 5, Appli  
30 38.5 47.5 1157 2 US-09-019-809-5 Sequence 5, Appli  
31 38.5 47.5 1157 2 US-09-471-177-5 Sequence 5, Appli  
32 38.5 47.5 1157 2 US-09-220-806-5 Sequence 5, Appli  
33 38 46.9 48 2 US-09-270-767-38395 Sequence 38395, A  
34 38 46.9 48 2 US-09-270-767-53612 Sequence 53612, A  
35 38 46.9 131 2 US-09-949-016-9319 Sequence 9319, Ap  
36 38 46.9 334 2 US-09-248-796A-19132 Sequence 19132, A  
37 38 46.9 485 2 US-09-489-039A-8129 Sequence 8129, Ap  
38 38 46.9 503 2 US-09-248-796A-15409 Sequence 15409, A  
39 38 46.9 769 2 US-10-191-436A-5 Sequence 5, Appli  
40 38 46.9 1155 2 US-09-710-279-1780 Sequence 1780, Ap  
41 38 46.9 1742 2 US-09-386-962C-4 Sequence 4, Appli  
42 38 46.9 1742 2 US-09-386-959-4 Sequence 4, Appli  
43 37 45.7 139 2 US-09-634-238-335 Sequence 335, App  
44 37 45.7 386 2 US-09-248-796A-21802 Sequence 21802, A  
45 37 45.7 420 2 US-09-844-006A-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-09-281-760E-37  
; Sequence 37, Application US/09281760E  
; Patent No. 6734287  
; GENERAL INFORMATION:  
; APPLICANT: Lawton, Robert  
; APPLICANT: Mermer, Brion  
; APPLICANT: Francoeur, Greg  
; TITLE OF INVENTION: Specific Binding Protein for Treating  
; TITLE OF INVENTION: Canine Allergy  
; FILE REFERENCE: 01-1275A  
; CURRENT APPLICATION NUMBER: US/09/281,760E  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: 09/058,331  
; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (136)..(136)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (413)..(414)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (451)..(451)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (460)..(462)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (500)..(500)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (530)..(530)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (568)..(568)  
; OTHER INFORMATION: "n" stands for any nucleic acid

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (847)..(849)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-37

Query Match      100.0%; Score 81; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTTG 15
Db 43 RNDSP1QTDQYTTTG 57

RESULT 2
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2

Query Match      100.0%; Score 81; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTTG 15
Db 255 RNDSP1QTDQYTTTG 269

RESULT 3
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.

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; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match      100.0%; Score 81; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTTG 15
Db 357 RNDSP1QTDQYTTTG 371

RESULT 4
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (908) 594-6734  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-13795-2

Query Match 100.0%; Score 81; DB 5; Length 426;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNDSPQTQDYTTG 15  
|||:|:|  
Db 357 RNDSPQTQDYTTG 371

RESULT 5  
US-09-479-614-14  
; Sequence 14, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-14

Query Match 59.3%; Score 48; DB 2; Length 431;  
Best Local Similarity 61.5%; Pred. No. 3.1;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTQDYTTT 14  
|||:|:|  
Db 363 NDSFVRTEQQATT 375

RESULT 6  
US-09-479-614-2  
; Sequence 2, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-2

Query Match 59.3%; Score 48; DB 2; Length 496;  
Best Local Similarity 61.5%; Pred. No. 3.6;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NDSPIQTQDYTTT 14  
|||:|:|  
Db 428 NDSFVRTEQQATT 440

RESULT 7  
US-09-479-614-29  
; Sequence 29, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-29

Query Match 59.3%; Score 48; DB 2; Length 496;  
Best Local Similarity 61.5%; Pred. No. 3.6;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTQDYTTT 14  
|||:|:|  
Db 428 NDSFVRTEQQATT 440

RESULT 8  
US-09-134-001C-4053  
; Sequence 4053, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4053  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4053

Query Match 50.8%; Score 41; DB 2; Length 533;  
Best Local Similarity 58.3%; Pred. No. 64;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTQDYTT 13  
||:|:|  
Db 466 NDAPQSDQIYT 477

RESULT 9  
US-09-270-767-43446  
; Sequence 43446, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:

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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43446
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43446

Query Match      49.4%; Score 40; DB 2; Length 163;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTT 14
   ||: ||: ||: ||: ||
Db 85 RNNEPLIADNYITT 98

RESULT 10
US-09-328-352-4294
; Sequence 4294, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4294
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4294

Query Match      49.4%; Score 40; DB 2; Length 667;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTQDQYTTT 14
   ||: ||: ||: ||: ||
Db 614 PLEADQYTTET 623

RESULT 11
US-09-206-942-65
; Sequence 65, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-65

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43446
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43446

Query Match      49.4%; Score 40; DB 2; Length 163;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTT 14
   ||: ||: ||: ||: ||
Db 85 RNNEPLIADNYITT 98

RESULT 10
US-09-328-352-4294
; Sequence 4294, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4294
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4294

Query Match      49.4%; Score 40; DB 2; Length 667;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTQDQYTTT 14
   ||: ||: ||: ||: ||
Db 614 PLEADQYTTET 623

RESULT 11
US-09-206-942-65
; Sequence 65, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-65
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Query Match      49.4%; Score 40; DB 2; Length 1180;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
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Db 13 RSDTNLENEYTG TG 27

RESULT 12
US-10-193-764-61
; Sequence 61, Application US/10193764
; Patent No. 6849447
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; FILE REFERENCE: 1038-1239MIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-61

Query Match      49.4%; Score 40; DB 2; Length 1180;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
   ||: ||: ||: ||: ||
Db 13 RSDTNLENEYTG TG 27

RESULT 13
US-09-206-942-63
; Sequence 63, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-63

Query Match      49.4%; Score 40; DB 2; Length 1188;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
   ||: ||: ||: ||: ||
Db 21 RSDTNLENEYTG TG 35
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RESULT 14  
 US-10-193-764-59  
 ; Sequence 59, Application US/10193764  
 ; Patent No. 6849447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loosmore, Sheena M.  
 ; APPLICANT: Yang, Yan-Ping  
 ; APPLICANT: Klein, Michel H.  
 ; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH  
 ; TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS  
 ; FILE REFERENCE: 1038-1239MIS  
 ; CURRENT APPLICATION NUMBER: US/10/193,764  
 ; CURRENT FILING DATE: 2002-07-12  
 ; PRIOR APPLICATION NUMBER: 09/167,568  
 ; PRIOR FILING DATE: 1998-10-07  
 ; NUMBER OF SEQ ID NOS: 91  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 59  
 ; LENGTH: 1188  
 ; TYPE: PRT  
 ; ORGANISM: Haemophilus influenzae  
 US-10-193-764-59

Query Match 49.4%; Score 40; DB 2; Length 1188;  
 Best Local Similarity 40.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPICQDQYTTTG 15  
 Db 21 RSDTNLENEYTG 35

RESULT 15  
 US-09-949-016-10828  
 ; Sequence 10828, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10828  
 ; LENGTH: 2186  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-949-016-10828

Query Match 49.4%; Score 40; DB 2; Length 2186;  
 Best Local Similarity 70.0%; Pred. No. 4.7e+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14  
 Db 1759 PLQSDQYTTT 1768

Search completed: August 30, 2006, 04:33:04  
 Job time : 15.8485 secs

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November 2005

Published\_Applications\_Nucleic Acid and Published\_Applications\_Amino Acid database searches now generate two sets of results each. The Published\_Applications\_databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_NA\_Main) and **.rapbn** (Published\_Applications\_NA\_New). Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

**This Page Blank (uspto)**

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 75.7576 Seconds  
(without alignments)  
91.717 Million cell updates/sec

Title: US-10-758-165a-1

Perfect score: 81

Sequence: 1 RNDSPQTQDQYTTTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.Main.\*

- 1: /EMC\_Celerra\_SID3S/ptodata/2/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /EMC\_Celerra\_SID3S/ptodata/2/pubpaa/US08\_PUBCOMB.pap.\*
- 3: /EMC\_Celerra\_SID3S/ptodata/2/pubpaa/US09\_PUBCOMB.pap.\*
- 4: /EMC\_Celerra\_SID3S/ptodata/2/pubpaa/US10A\_PUBCOMB.pap.\*
- 5: /EMC\_Celerra\_SID3S/ptodata/2/pubpaa/US10B\_PUBCOMB.pap.\*
- 6: /EMC\_Celerra\_SID3S/ptodata/2/pubpaa/US11\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	5	US-10-758-165-1
2	81	100.0	312	5	US-10-723-207-2
3	81	100.0	426	4	US-10-214-524-28
4	53	65.4	15	5	US-10-758-165-7
5	53	65.4	567	4	US-10-214-524-33
6	48	59.3	15	5	US-10-758-165-2
7	48	59.3	431	3	US-09-479-614-14
8	48	59.3	431	4	US-10-409-772-14
9	48	59.3	496	3	US-09-479-614-2
10	48	59.3	496	3	US-09-479-614-29
11	48	59.3	496	4	US-10-214-524-25
12	48	59.3	496	4	US-10-409-772-2
13	48	59.3	496	4	US-10-409-772-29
14	43	53.1	68	4	US-10-424-599-250413
15	43	53.1	1633	4	US-10-282-122A-70437
16	42	51.9	123	4	US-10-437-963-169489
17	42	51.9	161	4	US-10-425-115-238239
18	41	50.6	15	5	US-10-758-165-3
19	41	50.6	68	4	US-10-424-599-211575
20	41	50.6	191	4	US-10-767-701-39191
21	41	50.6	424	4	US-10-451-078-2
22	41	50.6	424	4	US-10-451-078-4
23	41	50.6	514	4	US-10-424-599-177658
24	41	50.6	534	4	US-10-724-972A-5049
25	41	50.6	569	4	US-10-214-524-30
26	40	49.4	356	6	US-11-097-143-19689
27	40	49.4	374	5	US-10-732-923-17586

Sequence 17624, A  
Sequence 355337, A  
Sequence 65347, A  
Sequence 135296,  
Sequence 4, Appli  
Sequence 44580, A  
Sequence 20346, A  
Sequence 50637, A  
Sequence 59, Appl  
Sequence 26, Appl  
Sequence 117513,  
Sequence 145953,

28 40 49.4 374 5 US-10-732-923-17624  
29 40 49.4 433 4 US-10-425-115-355337  
30 40 49.4 488 4 US-10-425-114-65347  
31 40 49.4 539 4 US-10-437-963-135296  
32 40 49.4 555 4 US-10-355-956-4  
33 40 49.4 555 5 US-10-504-048-4  
34 40 49.4 596 4 US-10-767-701-44580  
35 40 49.4 661 6 US-11-188-298-20346  
36 40 49.4 1180 4 US-10-193-764-61  
37 40 49.4 1188 4 US-10-193-764-59  
38 40 49.4 2400 5 US-10-450-763-50637  
39 40 49.4 2415 5 US-10-450-763-50638  
40 39 48.1 51 4 US-10-425-115-260566  
41 39 48.1 170 4 US-10-424-599-148645  
42 39 48.1 281 4 US-10-369-430A-26  
43 39 48.1 446 5 US-10-450-763-56495  
44 39 48.1 523 4 US-10-437-963-117513  
45 39 48.1 584 4 US-10-437-963-145953

#### ALIGNMENTS

##### RESULT 1

US-10-758-165-1

; Sequence 1, Application US/10758165

; Publication No. US20050196816A1

; GENERAL INFORMATION:

; APPLICANT: Hammerberg, Bruce

; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

; FILE REFERENCE: 5051-661

; CURRENT APPLICATION NUMBER: US/10758,165

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: US 60/440,472

; PRIOR FILING DATE: 2003-01-16

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 1

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Canis familiaris

US-10-758-165-1

Query Match 100.0%; Score 81; DB 5; Length 15;

Best Local Similarity 100.0%; Pred.No. 5.4e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15

Db 1 RNDSPQTQDQYTTTG 15

##### RESULT 2

US-10-723-207-2

; Sequence 2, Application US/10723207

; Publication No. US20050250934A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

; FILE REFERENCE: 1151-4153US2

; CURRENT APPLICATION NUMBER: US/10723,207

; CURRENT FILING DATE: 2003-11-24

; PRIOR APPLICATION NUMBER: 09/701,623

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US99/13959

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 09/100,287

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 2

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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match      100.0%; Score 81; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RNDSPQTDQYTTTG 15
Db      255 RNDSPQTDQYTTTG 269

RESULT 3
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match      100.0%; Score 81; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RNDSPQTDQYTTTG 15
Db      357 RNDSPQTDQYTTTG 371

RESULT 4
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match      65.4%; Score 53; DB 5; Length 15;
Best Local Similarity 57.1%; Pred. No. 0.039;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RNDSPQTDQYTTT 14
Db      1 RNDAPVQADRHSTT 14

RESULT 5
US-10-214-524-33
; Sequence 33, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Pig (Sus scrofa)
US-10-214-524-33

Query Match      65.4%; Score 53; DB 4; Length 567;
Best Local Similarity 57.1%; Pred. No. 2.1;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RNDSPQTDQYTTT 14
Db      499 RNDAPVQADRHSTT 512

RESULT 6
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match      59.3%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.29;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      2 NDSVPRTQQATT 14

RESULT 7
US-09-479-614-14
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; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match      59.3%; Score 48; DB 3; Length 431;
Best Local Similarity 61.5%; Pred. No. 12;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      363 NDSFVRTEQQATT 375

RESULT 8
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match      59.3%; Score 48; DB 4; Length 431;
Best Local Similarity 61.5%; Pred. No. 12;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      363 NDSFVRTEQQATT 375

RESULT 9
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match      59.3%; Score 48; DB 3; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      428 NDSFVRTEQQATT 440

RESULT 10
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match      59.3%; Score 48; DB 3; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      428 NDSFVRTEQQATT 440

RESULT 11
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match      59.3%; Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
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Db      428 NDSPVTEQQATT 440
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RESULT 12
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION: Catherine
; APPLICANT: McCall, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
Query Match      59.3%; Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPQTDQYTTT 14
||||:|:| ||
Db      428 NDSPVTEQQATT 440
||||:|:| ||
RESULT 13
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
Query Match      59.3%; Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPQTDQYTTT 14
||||:|:| ||
Db      428 NDSPVTEQQATT 440
||||:|:| ||
RESULT 14
US-10-424-599-250413
; Sequence 250413, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250413
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(68)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68150C.1.pep
US-10-424-599-250413
Query Match      53.1%; Score 43; DB 4; Length 68;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      4 SPIQTDQYTTTG 15
:| ||||| |
Db      21 TPRNTDQYTTIG 32
:| ||||| |
RESULT 15
US-10-282-122A-70437
; Sequence 70437, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70437
; LENGTH: 1633
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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70437

Query Match      53.1%; Score 43; DB 4; Length 1633;
Best Local Similarity 61.5%; Pred. No. 3.7e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14 .
Db      242 NDEPTQDVEYTTT 254
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Job time : 75.7576 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 7.72727 Seconds  
(without alignments)  
133.695 Million cell updates/sec

Title: US-10-758-165a-1

Perfect score: 81

Sequence: 1 RNSPTQTDQYTTTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pap:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pap:\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	41	50.6	462	US-10-953-349-22888	Sequence 22888, A
2	40	49.4	632	US-10-449-902-55064	Sequence 55064, A
3	40	49.4	661	US-11-330-403-15135	Sequence 15135, A
4	39	48.1	276	US-11-056-355B-36321	Sequence 36321, A
5	39	48.1	276	US-11-056-355B-103150	Sequence 103150, A
6	39	48.1	276	US-11-056-355B-114389	Sequence 114389, A
7	39	48.1	294	US-11-056-355B-36320	Sequence 36320, A
8	39	48.1	294	US-11-056-355B-103149	Sequence 103149, A
9	39	48.1	294	US-11-056-355B-114388	Sequence 114388, A
10	39	48.1	295	US-11-056-355B-36319	Sequence 36319, A
11	39	48.1	295	US-11-056-355B-103148	Sequence 103148, A
12	39	48.1	295	US-11-056-355B-114387	Sequence 114387, A
13	38	46.9	211	US-10-953-349-38543	Sequence 38543, A
14	38	46.9	294	US-10-953-349-38542	Sequence 38542, A
15	38	46.9	386	US-10-953-349-38541	Sequence 38541, A
16	38	46.9	1212	US-10-449-902-41189	Sequence 41189, A
17	38	46.9	1742	US-11-396-565-4	Sequence 4, Appl
18	37	45.7	162	US-10-449-902-41668	Sequence 41668, A
19	37	45.7	193	US-10-449-902-54797	Sequence 54797, A
20	37	45.7	335	US-11-056-355B-24060	Sequence 24060, A
21	37	45.7	335	US-11-056-355B-105306	Sequence 105306, A
22	37	45.7	335	US-11-056-355B-116545	Sequence 116545, A
23	37	45.7	379	US-10-449-902-40015	Sequence 40015, A
24	37	45.7	559	US-11-056-355B-78228	Sequence 78228, A
25	37	45.7	564	US-11-056-355B-91394	Sequence 91394, A

26	37	45.7	564	7	US-11-056-355B-95150	Sequence 95150, A
27	37	45.7	598	7	US-11-056-355B-78227	Sequence 78227, A
28	37	45.7	603	7	US-11-056-355B-91393	Sequence 91393, A
29	37	45.7	603	7	US-11-056-355B-95149	Sequence 95149, A
30	37	45.7	609	7	US-11-056-355B-78226	Sequence 78226, A
31	37	45.7	614	7	US-11-056-355B-91392	Sequence 91392, A
32	37	45.7	614	7	US-11-056-355B-95148	Sequence 95148, A
33	37	45.7	987	7	US-11-056-355B-74127	Sequence 74127, A
34	37	45.7	1016	7	US-11-070-573-17	Sequence 16, Appl
35	37	45.7	1016	7	US-11-070-573-17	Sequence 17, Appl
36	37	45.7	1071	7	US-11-056-355B-74126	Sequence 74126, A
37	37	45.7	1160	7	US-11-056-355B-74125	Sequence 74125, A
38	37	45.7	1743	7	US-11-248-956-32	Sequence 32, Appl
39	36	44.4	140	7	US-11-056-355B-8760	Sequence 8760, Ap
40	36	44.4	174	7	US-11-056-355B-8759	Sequence 8759, Ap
41	36	44.4	189	7	US-11-174-307B-4644	Sequence 4644, Ap
42	36	44.4	191	7	US-11-056-355B-8758	Sequence 8758, Ap
43	36	44.4	252	7	US-11-056-355B-47040	Sequence 47040, A
44	36	44.4	292	6	US-10-471-571A-3346	Sequence 3346, Ap
45	36	44.4	292	7	US-11-056-355B-13017	Sequence 13017, A

ALIGNMENTS

RESULT 1  
US-10-953-349-22888  
; Sequence 22888, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953.349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22888  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-22888

Query Match 50.6%; Score 41; DB 6; Length 462;  
Best Local Similarity 63.6%; Pred. No. 17;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 5 PIQTDQYTTTG 15  
| | | | |  
Db 12 PSQTDRENTTG 22

RESULT 2  
US-10-449-902-55064  
; Sequence 55064, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 55064

; LENGTH: 632  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-55064

Query Match 49.4%; Score 40; DB 6; Length 632;  
Best Local Similarity 60.0%; Pred. No. 35;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQY 11  
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Db 231 NDEPLQEQY 240

## RESULT 3

US-11-330-403-15135  
; Sequence 15135, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 15135

; LENGTH: 661  
; TYPE: PRT  
; ORGANISM: Bacillus cereus ATCC 14579

US-11-330-403-15135

Query Match 49.4%; Score 40; DB 7; Length 661;  
Best Local Similarity 69.2%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
|||:|:|:  
Db 569 NDSIKVDTYTTT 581

## RESULT 4

US-11-056-355B-36321  
; Sequence 36321, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 36321

; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana

; NAME/KEY: peptide  
; LOCATION: (1)...(276)  
; OTHER INFORMATION: Ceres Seq. ID no. 12321429

US-11-056-355B-36321

Query Match 48.1%; Score 39; DB 7; Length 276;  
Best Local Similarity 75.0%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11  
:|:|:|:  
Db 183 APVQTDQY 190

## RESULT 5

US-11-056-355B-103150  
; Sequence 103150, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 103150

; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana

; NAME/KEY: peptide  
; LOCATION: (1)..(276)  
; OTHER INFORMATION: Ceres Seq. ID no. 13612112

US-11-056-355B-103150

Query Match 48.1%; Score 39; DB 7; Length 276;  
Best Local Similarity 75.0%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11  
:|:|:|:  
Db 183 APVQTDQY 190

## RESULT 6

US-11-056-355B-114389  
; Sequence 114389, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 114389

; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana

; NAME/KEY: peptide  
; LOCATION: (1)..(276)  
; OTHER INFORMATION: Ceres Seq. ID no. 13612112

US-11-056-355B-114389

Query Match 48.1%; Score 39; DB 7; Length 276;  
Best Local Similarity 75.0%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11  
:|:|:|:  
Db 183 APVQTDQY 190

## RESULT 7

US-11-056-355B-36320  
; Sequence 36320, Application US/11056355B  
; Publication No. US20060150283A1

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; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 114388
; LENGTH: 294
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 13612111
US-11-056-355B-114388

Query Match      48.1%; Score 39; DB 7; Length 294;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      201 APVQTDQY 208

RESULT 10
US-11-056-355B-36319
; Sequence 36319, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36319
; LENGTH: 295
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(295)
; OTHER INFORMATION: Ceres Seq. ID no. 12321427
US-11-056-355B-36319

Query Match      48.1%; Score 39; DB 7; Length 295;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      202 APVQTDQY 209

RESULT 11
US-11-056-355B-103148
; Sequence 103148, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13

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; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 103148  
; LENGTH: 295  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(295)  
; OTHER INFORMATION: Ceres Seq. ID no. 13612110  
US-11-056-355B-103148

Query Match 48.1%; Score 39; DB 7; Length 295;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11  
:|:|:|:|  
Db 202 APVQTDQY 209

## RESULT 12

US-11-056-355B-114387  
; Sequence 114387, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/11/056.355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 114387  
; LENGTH: 295  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(295)  
; OTHER INFORMATION: Ceres Seq. ID no. 13612110  
US-11-056-355B-114387

Query Match 48.1%; Score 39; DB 7; Length 295;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11  
:|:|:|:|  
Db 202 APVQTDQY 209

## RESULT 13

US-10-953-349-38543  
; Sequence 38543, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953.349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 38543  
; LENGTH: 211  
; TYPE: PRP  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-38543

Query Match 46.9%; Score 38; DB 6; Length 211;  
Best Local Similarity 46.7%; Pred. No. 24;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15  
:|:|:|:|  
Db 66 RQEPPEQIDRYRTVG 80

## RESULT 14

US-10-953-349-38542  
; Sequence 38542, Application US/109533349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953.349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 38542  
; LENGTH: 294  
; TYPE: PRP  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-38542

Query Match 46.9%; Score 38; DB 6; Length 294;  
Best Local Similarity 46.7%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15  
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Db 149 RQEPPEQIDRYRTVG 163

## RESULT 15

US-10-953-349-38541  
; Sequence 38541, Application US/109533349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953.349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 38541  
; LENGTH: 386  
; TYPE: PRP  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-38541

Query Match 46.9%; Score 38; DB 6; Length 386;  
Best Local Similarity 46.7%; Pred. No. 47;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15  
:|:|:|:|  
Db 241 RQEPPEQIDRYRTVG 255

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Job time : 7.72727 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 54.5455 Seconds  
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Title: US-10-758-165a-2  
Perfect score: 85  
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Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	85	100.0	431	8 ADG73237	Adg73237 Cat immun
3	85	100.0	496	6 ABP96580	Abp96580 Cat IGE h
4	85	100.0	496	6 ABU09338	Abu09338 Feline Ig
5	85	100.0	496	6 ABU09336	Abu09336 Feline Ig
6	85	100.0	496	8 ADG73251	Adg73251 Cat parti
7	85	100.0	496	8 ADG73225	Adg73225 Cat parti
8	48	56.5	15	8 ADR10601	Adr10601 Dog IGE e
9	48	56.5	312	3 AAY79995	Aay79995 Dog immun
10	48	56.5	417	2 AAW23067	Aaw23067 Canine Ig
11	48	56.5	426	2 AAR97753	Aar97753 Canine Ig
12	48	56.5	426	6 ABP96583	Abp96583 Dog IGE h
13	47	55.3	84	6 ABU55745	Abu55745 Tree cott
14	46	54.1	449	4 ABB60974	Abb60974 Drosophil
15	45	52.9	321	4 AAE12007	Aae12007 Streptomy
16	45	52.9	321	6 ABG73760	Abg73760 S. cattle
17	44	51.8	673	4 ABB71738	Abb71738 Drosophil
18	43	50.6	470	8 ADS27897	Ads27897 Bacterial
19	43	50.6	696	8 ADX67175	Adx67175 Plant ful
20	42	49.4	87	4 AAU55966	Aau55966 Propionib
21	42	49.4	87	6 ABM52485	Abm52485 Propionib
22	42	49.4	178	5 ABB83494	Abb83494 Human zin
23	42	49.4	178	7 ADB65732	Adb65732 Human pro

24	42	49.4	197	8 ABO60445	AbO60445 Human gen
25	42	49.4	296	6 ADA54799	Ada54799 Human pro
26	42	49.4	296	7 AAO27216	Aao27216 Human zin
27	42	49.4	349	4 AAM79729	Aam79729 Human pro
28	42	49.4	430	4 AAM78745	Aam78745 Human pro
29	42	49.4	536	9 ADY18750	Ady18750 PRO polyp
30	42	49.4	537	6 AAE33775	Aae33775 Human nuc
31	41	48.2	70	4 AAU59982	Aau59982 Propionib
32	41	48.2	70	6 ABM56501	Abm56501 Propionib
33	41	48.2	152	4 AAM18098	Aam18098 Peptide #
34	41	48.2	152	4 ABB37133	Abb37133 Peptide #
35	41	48.2	152	4 AAM30608	Aam30608 Peptide #
36	41	48.2	152	4 ABB22444	Abb22444 Protein #
37	41	48.2	152	4 AAM70271	Aam70271 Human don
38	41	48.2	152	4 AAM57851	Aam57851 Human bra
39	41	48.2	152	4 AAM05733	Aam05733 Peptide #
40	41	48.2	349	4 AAU30476	Aau30476 Novel hum
41	41	48.2	381	9 AED71188	Aed71188 Corynebac
42	41	48.2	534	9 AED71186	Aed71186 Corynebac
43	41	48.2	647	4 AAG92695	Aag92695 C glutami
44	41	48.2	812	4 ABG19065	Abg19065 Novel hum
45	41	48.2	1194	8 ADP29882	Adp29882 Human sec

ALIGNMENTS

RESULT 1  
ADRI0602  
ID ADR10602 standard; peptide; 15 AA.  
XX  
AC ADR10602;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.  
XX  
KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW cat.  
XX  
OS Felis catus.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX Hammerberg B;  
XX WPI; 2004-593545/57.  
PT Novel antibody that specifically binds to mammalian IgE epitope, useful  
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian IgE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. (I) is also useful for detecting mammalian IgE and for  
CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the

CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC cat IgE 5.91 recognition site.  
 XX  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15  
 |||||  
 Db 1 HNDSPVTEQQATTW 15

## RESULT 2

ADG73237  
 ID ADG73237 standard; protein; 431 AA.

XX AC ADG73237;

XX 11-MAR-2004 (first entry)

XX Cat immunoglobulin E (IgE) constant region.

XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;  
 KW immune response; IgE-mediated response; allergy; cat; constant region.  
 XX  
 XX Felis catus.

OS US2003216565-A1.

FN 20-NOV-2003.

XX 07-APR-2003; 2003US-00409772.

XX 07-JAN-1999; 99US-0115033P.

PR 07-JAN-2000; 2000US-00479614.

XX (MCCA/) MCCALL C.

FA (WEBER/) WEBER E.

XX McCall C, Weber E;

XX WPI; 2004-010802/01.

DR N-PSDB; ADG73236.

XX New isolated nucleic acid molecule encoding a portion of a feline IgE  
 PT heavy chain protein, useful for treating and/or eliciting feline immune  
 PT responses for IgE-mediated responses, such as allergies.

PS Claim 12; SEQ ID NO 14; 44pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a  
 CC portion of a feline IgE heavy chain protein. The methods and compositions  
 CC of the present invention are useful for eliciting feline immune responses  
 CC for and/or treating IgE-mediated responses, such as allergies. This is  
 CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.  
 XX

SQ Sequence 431 AA;

Query Match 100.0%; Score 85; DB 8; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15  
 |||||  
 Db 362 HNDSPVTEQQATTW 376

## RESULT 3

ABP96580

ID ABP96580 standard; protein; 496 AA.

XX AC ABP96580;

XX 28-MAY-2003 (first entry)

DE Cat IgE heavy chain amino acid sequence SEQ ID NO:25.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
 KW immune response; major histocompatibility complex; MHC; immunogenic;  
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.

XX Felis catus.

XX W02003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IgE, by identifying peptide eliciting CTL response to IgE  
 PT peptides naturally presented by major histocompatibility complex class I  
 PT protein.

PS Example 7; Page 145-147; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IgE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,  
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in  
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic  
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an IgE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention

XX Sequence 496 AA;

Query Match 100.0%; Score 85; DB 6; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15

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Db      427 HNDSPVTEQQATTW 441
|||||
RESULT 4
ABU09338
ID ABU09338 standard; protein; 496 AA.
XX
AC ABU09338;
XX
XX 27-JUN-2003 (first entry)
XX
XX Feline IgE epsilon heavy chain #2.
XX
XX Feline, immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
KW IgE-mediated immune response; allergy; neoplasia; vaccine technology;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
XX Felis catus.
XX
XX US2003013183-A1.
XX
XX 16-JAN-2003.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX (MCCA/) MCCALL C.
XX (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2003-391997/37.
XX N-PSDB; ABX95715.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
XX Claim 1; Page 37-39; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #2
XX
XX Sequence 496 AA;
XX
Query Match 100.0%; Score 85; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNDSPVTEQQATTW 15
|||||
Db 427 HNDSPVTEQQATTW 441
|||||
RESULT 5
ABU09336
ID ABU09336 standard; protein; 496 AA.
XX
AC ABU09336;
XX
XX 27-JUN-2003 (first entry)
XX
XX Feline IgE epsilon heavy chain #1.
XX
XX Feline, immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
KW

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KW IgE-mediated immune response; allergy; neoplasia; vaccine technology;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
XX Felis catus.
XX
XX Location/Qualifiers
FH Key 66..496
FT Region /note= "This sequence is given as SEQ ID No:14 and is
FT specifically claimed in Claim 12"
FT Region 284..309
FT /note= "This sequence is given as SEQ ID No:11 and is
FT specifically claimed in Claim 9"
FT Region 288..305
FT /note= "This sequence is given as SEQ ID No:8 and is
FT specifically claimed in Claim 10"
FT Region 291..302
FT /note= "This sequence is given as SEQ ID No:5 and is
FT specifically claimed in Claim 11"
XX
XX US2003013183-A1.
XX
XX 16-JAN-2003.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX (MCCA/) MCCALL C.
XX (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2003-391997/37.
XX N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
XX Claim 1; Page 24-25; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #1
XX
XX Sequence 496 AA;
XX
Query Match 100.0%; Score 85; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNDSPVTEQQATTW 15
|||||
Db 427 HNDSPVTEQQATTW 441
|||||
RESULT 6
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
AC ADG73251;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat partial immunoglobulin E (IgE) heavy chain #2.
XX
XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
KW immune response; IgE-mediated response; allergy; cat; heavy chain.

```

```

XX OS Felis catus.
XX PN US2003216565-A1.
XX XX 20-NOV-2003.
XX PD
XX XX
XX PF 07-APR-2003; 2003US-00409772.
XX XX
XX PR 07-JAN-1999; 99US-0115033P.
XX PR 07-JAN-2000; 2000US-00479614.
XX XX
XX XX (MCCA/) MCCALL C.
XX PA (WEBE/) WEBER E.
XX XX
XX PI McCall C, Weber E;
XX XX
XX DR WPI; 2004-010802/01.
XX DR N-PSDB; ADG73225.
XX XX
XX XX New isolated nucleic acid molecule encoding a portion of a feline IgE
XX PT heavy chain protein, useful for treating and/or eliciting feline immune
XX PT responses for IGE-mediated responses, such as allergies.
XX XX
XX PS Claim 8; SEQ ID NO 29; 44pp; English.
XX XX
XX CC The invention describes an isolated nucleic acid molecule (I) encoding a
XX CC portion of a feline IgE heavy chain protein. The methods and compositions
XX CC of the present invention are useful for eliciting feline immune responses
XX CC for and/or treating IGE-mediated responses, such as allergies. This is
XX CC the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
XX CC chain.
XX XX
XX SQ Sequence 496 AA;
XX
XX Query Match 100.0%; Score 85; DB 8; Length 496;
XX Best Local Similarity 100.0%; Pred. No. 3e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HNDSPVRTEQQATTW 15
XX |||||||||||
XX DB 427 HNDSPVRTEQQATTW 441
XX
XX RESULT 7
XX ADG73225
XX ID ADG73225 standard; protein; 496 AA.
XX XX
XX AC ADG73225;
XX XX
XX DT 11-MAR-2004 (first entry)
XX XX
XX DE Cat partial immunoglobulin E (IgE) heavy chain #1.
XX XX
XX KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
XX KW immune response; IGE-mediated response; allergy; cat; heavy chain.
XX XX
XX OS Felis catus.
XX XX
XX PN US2003216565-A1.
XX XX
XX PD 20-NOV-2003.
XX XX
XX PF 07-APR-2003; 2003US-00409772.
XX XX
XX PR 07-JAN-1999; 99US-0115033P.
XX PR 07-JAN-2000; 2000US-00479614.
XX XX
XX XX (MCCA/) MCCALL C.
XX PA (WEBE/) WEBER E.
XX XX
XX PI McCall C, Weber E;
XX XX
XX DR WPI; 2004-010802/01.
XX DR N-PSDB; ADG73225.
XX XX
XX XX New isolated nucleic acid molecule encoding a portion of a feline IgE
XX PT heavy chain protein, useful for treating and/or eliciting feline immune
XX PT responses for IGE-mediated responses, such as allergies.
XX XX
XX PS Claim 8; SEQ ID NO 29; 44pp; English.
XX XX
XX CC The invention describes an isolated nucleic acid molecule (I) encoding a
XX CC portion of a feline IgE heavy chain protein. The methods and compositions
XX CC of the present invention are useful for eliciting feline immune responses
XX CC for and/or treating IGE-mediated responses, such as allergies. This is
XX CC the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
XX CC chain.
XX XX
XX SQ Sequence 496 AA;
XX
XX Query Match 100.0%; Score 85; DB 8; Length 496;
XX Best Local Similarity 100.0%; Pred. No. 3e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HNDSPVRTEQQATTW 15
XX |||||||||||
XX DB 427 HNDSPVRTEQQATTW 441
XX
XX RESULT 8
XX ADRI0601
XX ID ADRI0601 standard; peptide; 15 AA.
XX XX
XX AC ADRI0601;
XX XX
XX DT 21-OCT-2004 (first entry)
XX XX
XX DE Dog IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
XX XX
XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX XX
XX OS Canis familiaris.
XX XX
XX PN WO2004065936-A2.
XX XX
XX PD 05-AUG-2004.
XX XX
XX PF 15-JAN-2004; 2004WO-US003566.
XX XX
XX PR 16-JAN-2003; 2003US-0440472P.
XX XX
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX XX
XX PI Hammerberg B;
XX XX
XX XX WPI; 2004-593545/57.
XX XX
XX XX Novel antibody that specifically binds to mammalian IgE epitope, useful
XX PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
XX PT or treating asthma or anaphylactic shock.
XX XX
XX PS Example 6; Page 9; 14pp; English.
XX XX
XX CC The present invention relates to a novel monoclonal antibody (I) that
XX CC specifically binds to a mammalian IgE epitope, where the epitope is
XX CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
XX CC (I) is useful for testing an allergen reactivity of an IgE sample. The
XX CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX CC and corn allergens. The sample is a biological sample collected from a
XX CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
XX CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX CC antibodies recognise epitopes on canine IgE corresponding to amino acid
XX CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from

```



CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.  
 XX  
 SQ Sequence 15 AA;

Query Match 56.5%; Score 48; DB 8; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 0.24;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVRTEQQATT 14  
 ||||:|:|  
 Db 2 NDSPIQTDQYTTT 14

RESULT 9  
 AAY79995  
 ID AAY79995 standard; protein; 312 AA.  
 XX  
 AC AAY79995;  
 XX  
 DT 15-MAY-2000 (first entry)  
 XX  
 DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.  
 XX  
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.  
 XX  
 OS Canis sp.  
 XX  
 XX WO9967293-A1.  
 XX  
 XX 29-DEC-1999.  
 XX  
 XX 21-JUN-1999; 99WO-US013959.  
 XX  
 XX 20-JUN-1998; 98US-00100287.  
 XX  
 XX (UNBI-) UNITED BIOMEDICAL INC.  
 XX  
 XX Wang CY, Walfield AM;  
 XX  
 XX WPI; 2000-160578/14.  
 XX  
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 XX for immunization against allergy.  
 XX  
 XX Example 1; Page 66-68; 155pp; English.  
 XX  
 CC The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 312 AA;

Query Match 56.5%; Score 48; DB 3; Length 312;

Best Local Similarity 61.5%; Pred. No. 7.4;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVRTEQQATT 14  
 ||||:|:|  
 Db 256 NDSPIQTDQYTTT 268

RESULT 10  
 AAW23067  
 ID AAW23067 standard; protein; 417 AA.  
 XX  
 AC AAW23067;  
 XX  
 DT 30-JUN-2005 (revised)  
 DT 16-JUN-2005 (revised)  
 DT 19-FEB-1998 (first entry)  
 XX  
 DE Canine IgE heavy chain constant region (exon 1-4 product).  
 XX  
 KW IgE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.  
 XX  
 OS Canis familiaris.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 55 /note= "encoded by ACC"  
 FT Misc-difference 56 /note= "encoded by TAC"  
 FT Misc-difference 67 /note= "encoded by GCC"  
 FT Misc-difference 83 /note= "encoded by NNT"  
 FT Misc-difference 174 /note= "encoded by GGN"  
 FT Misc-difference 175 /note= "encoded by NNG"  
 FT Misc-difference 176 /note= "encoded by TGN"  
 FT Misc-difference 203 /note= "encoded by TCC"  
 FT Misc-difference 204 /note= "encoded by GAC"  
 FT  
 XX WO9730156-A2.  
 XX  
 XX 21-AUG-1997.  
 XX  
 XX 14-FEB-1997; 97WO-US002322.  
 XX  
 XX 14-FEB-1996; 96US-00601197.  
 XX  
 XX (IDEX-) IDEXX LAB INC.  
 XX  
 XX Mermer B, Harris RA, Siefing AE;  
 XX  
 XX WPI; 1997-425031/39.  
 XX N-PSDB; AAT79278.  
 XX  
 XX Isolated canine IgE heavy chain constant region DNA - useful to develop  
 XX products for treatment of canine allergies and for immunomodulation in  
 XX dogs.  
 XX  
 XX Disclosure; Page 35-39; 59pp; English.  
 XX  
 XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE  
 XX heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 XX comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 XX peptides encoded by exons 1-6 can be produced in eukaryotic or  
 XX prokaryotic cells. Such peptides, and antibodies raised against them, are  
 XX used in methods to treat the manifestation of allergy in dogs, e.g. to  
 XX treat Type I immediate hypersensitivity, and for immunomodulation

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CC CC Revised record issued on 30-JUN-2005 : Typo in comments
XX SQ Sequence 417 AA;

Query Match          56.5%; Score 48; DB 2; Length 417;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14
Db 353 NDSPIQTDQYTTT 365

RESULT 11
ID AAR97753 standard; protein; 426 AA.
XX AC AAR97753;
XX DT 28-AUG-1996 (first entry)
XX DE Canine IGE.
XX KW IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX OS Canis familiaris.
XX PN WO9614867-A1.
XX PD 23-MAY-1996.
XX PF 03-NOV-1995; 95WO-US013795.
XX PR 09-NOV-1994; 94US-00336583.
XX PR 09-NOV-1994; 94US-00336891.
XX PA (MERI ) MERCK & CO INC.
XX PI Hollis GF, Patel MD;
XX DR WPI; 1996-277321/28.
XX DR N-PSDB; RAT29824.
XX PT New DNA encoding canine IGE and IgA - useful in vaccines, anti-sense
XX PS therapy, assays, drug screening, etc.
XX PS Claim 11; Page 29-30; 49pp; English.
XX CC The canine IGE amino acid sequence (AAR97753) was deduced from an
XX CC isolated gene (AAR29824) obt'd. from a canine liver DNA library. The
XX CC cloning of the IGE gene allows prodn. of large quantities of recombinant
XX CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE
XX CC can be used in drug development (e.g. small molecule screening, assay
XX CC development and anti-IGE antibody generation). Fragments of IGE can be
XX CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new
XX CC sequence information permits targeted modulation of IGE-mediated immune
XX CC responses
XX SQ Sequence 426 AA;

Query Match          56.5%; Score 48; DB 2; Length 426;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14
Db 358 NDSPIQTDQYTTT 370

RESULT 12
ID ABP96583 standard; protein; 426 AA.

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```

XX ABP96583;
XX AC 28-MAY-2003 (first entry)
XX DT Dog IGE heavy chain amino acid sequence SEQ ID NO:28.
XX DE Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
XX KW immune response; major histocompatibility complex; MHC; immunogenic;
XX KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
XX KW dermatologic; antiinflammatory; IGE-mediated condition; food allergy;
XX KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX KW urticaria hives.
XX OS Canis familiaris.
XX PN WO2003015716-A2.
XX PD 27-FEB-2003.
XX PF 08-AUG-2002; 2002WO-US026986.
XX PR 13-AUG-2001; 2001US-0312120P.
XX PA (IGET-) IGE THERAPEUTICS INC.
XX PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX DR WPI; 2003-268242/26.
XX PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
XX PT against IGE, by identifying peptide eliciting CTL response to IGE
XX PT peptides naturally presented by major histocompatibility complex class I
XX PS protein.
XX PS Example 7; Page 152-154; 187pp; English.
XX CC The present invention describes a method (M1) for identifying peptides
XX CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
XX CC E (IGE), comprising providing a test peptide (T) suspected of being able
XX CC to bind to major histocompatibility complex (MHC) class I molecule, and
XX CC evaluating (T) for ability to elicit in a mammal a CTL response to
XX CC naturally processed and presented IGE peptides, where a peptide that
XX CC induces such a response is identified. Also described are compositions:
XX CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
XX CC (C2) comprising at least one isolated polynucleotide encoding (I); and
XX CC (C3) comprising antigen-presenting cells that recognise at least one (I).
XX CC Where C1-3 are able to bind to at least one MHC class I molecule and to
XX CC elicit in a mammal a CTL response to naturally processed and presented
XX CC IGE peptides, C1-3 have antiallergic, antiasthmatic, immunosuppressive,
XX CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
XX CC and can be used as inducers of a CTL response against IGE, and in
XX CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
XX CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
XX CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
XX CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
XX CC useful for treating atopic hypersensitivity conditions (such as allergic
XX CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
XX CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
XX CC hives). The present sequence represents an IGE heavy chain amino acid
XX CC sequence, which is given in an example from the present invention
XX SQ Sequence 426 AA;

Query Match          56.5%; Score 48; DB 6; Length 426;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14
Db 358 NDSPIQTDQYTTT 370

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RESULT 13  
ABU55745  
ID ABU55745 standard; protein; 84 AA.  
XX AC ABU55745;  
XX DT 17-MAR-2003 (first entry)  
XX DE Tree cotton growth regulating protein, GaGREP1.  
XX KW ss; plant; growth regulating protein; PSK; phyto sulphokine-alpha;  
XX KW transgenic; marker-assisted breeding; agriculture; horticulture.  
XX OS Gossypium arboreum.  
XX FN WO200283901-A2.  
XX PD 24-OCT-2002.  
XX PF 11-APR-2002; 2002WO-EP004035.  
XX PR 12-APR-2001; 2001US-0283313P.  
XX PA (CROP-) CROPEDESIGN NV.  
XX PA (SAUT/) SAUTER M.  
XX PI Sauter M, Lorbiecke R, Mironov V, Frankard V, Dillen W;  
XX PI Lejeune P, Broekaert W;  
XX XX  
XX DR WPI; 2003-093023/08.  
XX DR N-PSDB; ABX74222.  
XX PT New isolated GREP nucleic acids and polypeptides controlling or modifying  
XX PT the growth characteristics of a plant, useful for a wide application in  
XX PT agricultural and horticultural practices, and in vitro plant cell and  
XX PT tissue culture.  
XX PS Claim 5; Fig 22; 156pp; English.  
XX CC The invention relates to a new isolated nucleic acid encoding a growth  
XX CC regulating protein (GREP), where the protein conforms to the GREP  
XX CC signature sequence appearing as ABU55742, and the GREP proteins. Also  
XX CC included are a vector comprising a GREP nucleic acid, or a vector  
XX CC encoding the rice growth regulating polypeptide OsPSK (phyto sulphokine-  
XX CC alpha) where the growth regulating proteins regulate growth and/or  
XX CC development response in intact plants, a GREP transgenic plant, a  
XX CC transgenic plant comprising the vector, seed/pollen and a harvestable  
XX CC part of propagation material from the transgenic plant, a host cell  
XX CC comprising the GREP nucleic acid, an antisense molecule consisting of 14-  
XX CC 100 nucleotides targeted to the GREP signature nucleotide sequence  
XX CC appearing as ABX74197, an anti-GREP antibody which specifically  
XX CC recognises a GREP or its fragment, a method for altering growth and/or  
XX CC activity of a plant or plant cell/storage organ comprising modulating the  
XX CC level and/or activity of a GREP or the rice growth regulating peptide  
XX CC OsPSK, a method for downregulating levels of a GREP or OsPSK gene product  
XX CC or its activity (comprising administering or exposing GREP or OsPSK  
XX CC antibodies or gene products to cells, tissues or organs of a plant) a  
XX CC method for identifying an allele with desired features of a gene encoding  
XX CC a GREP which comprises isolating alleles for a GREP and testing the  
XX CC features of the allele by expression in a transgenic plant, a method for  
XX CC identifying an allele of GREP and selecting an allele with desired  
XX CC features which comprises the use of genes encoding GREP, or sequences  
XX CC located in the genome in the neighbourhood of GREP genes, as molecular  
XX CC markers for different GREP alleles and selecting specific GREP alleles by  
XX CC marker-assisted breeding and a method for identifying regulatory  
XX CC sequences of GREP growth regulating polypeptide genes. The methods and  
XX CC compositions are for controlling or modifying the growth characteristics  
XX CC of a plant or its organs and tissues, useful for a wide application in  
XX CC agricultural and horticultural practices, and in vitro plant cell and  
XX CC tissue culture. The present sequence is a growth regulating protein  
XX CC Sequence 84 AA;  
XX  
Query Match 55.3%; Score 47; DB 6; Length 84;  
Best Local Similarity 61.5%; Pred. No. 2.6;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NDSFVRTEQQATT 14  
DB 32 NDSFVKTQSOGTT 44  
RESULT 14  
ABB60974  
ID ABB60974 standard; protein; 449 AA.  
XX AC ABB60974;  
XX DT 26-MAR-2002 (first entry)  
XX DE Drosophila melanogaster polypeptide SEQ ID NO 9714.  
XX KW Drosophila; developmental biology; cell signalling; insecticide;  
XX KW pharmaceutical.  
XX OS Drosophila melanogaster.  
XX PN WO200171042-A2.  
XX PD 27-SEP-2001.  
XX PF 23-MAR-2001; 2001WO-US009231.  
XX PR 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX PA (PEKE ) PE CORP NY.  
XX PI Venter JC, Adams M, Li PWD, Myers EW;  
XX DR WPI; 2001-656860/75.  
XX DR N-PSDB; ABL05077.  
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell  
XX PT interactions.  
XX PS Disclosure; SEQ ID NO 9714; 21pp + Sequence Listing; English.  
XX CC The invention relates to an isolated nucleic acid detection reagent  
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is  
XX CC useful in developmental biology and in elucidating cell signalling and  
XX CC cell-cell interactions in higher eukaryotes for the development of  
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention  
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (AB557737-  
XX CC AB572072). The sequence data for this patent did not form part of the  
XX CC printed specification, but was obtained in electronic format directly  
XX CC from WIPO at fip.wipo.int/pub/published\_pct\_sequences  
XX CC Sequence 449 AA;  
XX  
Query Match 54.1%; Score 46; DB 4; Length 449;  
Best Local Similarity 53.3%; Pred. No. 25;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 HNDSPVRTEQQATTW 15  
DB 133 HNDGFVRCPEALTW 147  
RESULT 15  
AAE12007  
ID AAE12007 standard; protein; 321 AA.  
XX XX

AC AAE12007;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Streptomyces cattleya modified isopenicillin N synthetase (IPNS).  
XX  
KW Isopenicillin N synthetase; IPNS; antibiotic; penicillin; oxygenase;  
KW non-haeme iron (II) dependent family; oxidase; mutant; mutein.  
XX  
OS Streptomyces cattleya.  
OS  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 211  
FT /note= "Wild type Glu substituted with Arg"  
XX  
XX US6284483-B1.  
XX  
XX 04-SEP-2001.  
XX  
XX 06-OCT-1999; 99US-00413231.  
XX  
XX 06-OCT-1999; 99US-00413231.  
XX  
XX (UNMS ) UNIV MICHIGAN STATE.  
XX  
XX Dilley DR, Kadyrzhanova DK, Wang Z, Warner TM;  
XX WPI; 2001-615433/71.  
XX  
XX Method for producing antibiotics, particularly penicillin G or V,  
XX comprises employing a modified isopenicillin N synthetase, in either an  
XX organism or a cell-free system under the control of bicarbonate.  
XX  
XX Claim 2; Col 37-38; 27pp; English.  
XX  
XX The invention relates to a modified enzyme of a non-haeme iron (II)  
XX dependent family of oxygenases and oxidases which renders the enzyme  
XX dependent on bicarbonate for activity. The invention also related to a  
XX method for producing penicillin G or V comprises employing a modified  
XX enzyme, particularly isopenicillin N synthetase (IPNS), in either an  
XX organism or a cell-free system, under the control of bicarbonate. The  
XX modified enzymes are IPNS, deacetoxycephalosporin C synthetase (DAOCS)  
XX and deacetylcephalosporin C synthetase (DACS). The method is useful for  
XX producing antibiotics, particularly penicillin G or V. The method is  
XX useful for making organisms useful for making an antibiotic dependent on  
XX bicarbonate to make the antibiotic. The present sequence is Streptomyces  
XX cattleya modified isopenicillin N synthetase showing an Arg211 in place  
XX of Glu211  
XX  
SQ Sequence 321 AA;  
Query Match 52.9%; Score 45; DB 4; Length 321;  
Best Local Similarity 50.0%; Pred. No. 26;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NDSVPRTEQQATW 15  
|:| |:|  
Db 61 NESTMTDQSRSTW 74

Search completed: August 30, 2006, 04:22:04  
Job time : 56.5455 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 8.93939 Seconds  
(without alignments)  
161.448 Million cell updates/sec

Title: US-10-758-165a-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\* \*  
1: Piri:\*  
2: Piri2:\*  
3: Piri3:\*  
4: Piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	52.9	321	2 A58458	isopenicillin N sy
2	43.5	51.2	403	2 JC5171	D-galactose-bindin
3	43	50.6	375	2 S58484	gag protein - maiz
4	43	50.6	470	2 D87485	glutamyl-tRNA synt
5	42	49.4	247	2 AF2006	hypothetical prote
6	42	49.4	283	2 B49348	succinoglycan bios
7	42	49.4	319	2 A95976	glucosyltransferas
8	42	49.4	319	2 S40175	ExoW protein - Rhi
9	41	48.2	101	2 B97851	hypothetical prote
10	41	48.2	259	2 B85066	hypothetical prote
11	41	48.2	1449	2 T20181	hypothetical prote
12	41	48.2	1584	2 T20180	hypothetical prote
13	41	48.2	1586	2 T20179	hypothetical prote
14	40	47.1	151	2 AF0931	probable exported
15	40	47.1	270	2 F64050	glucosamine-6-phos
16	40	47.1	275	2 S21348	probable pol polyp
17	40	47.1	410	2 D87151	probable integral
18	40	47.1	513	2 S21976	probable RNA-direc
19	40	47.1	557	2 AB0204	methyl-accepting c
20	40	47.1	631	2 D71933	hypothetical prote
21	40	47.1	635	2 D84855	probable seed natu
22	39	45.9	88	2 A38112	hipB protein - Esc
23	39	45.9	113	2 C31769	T-cell receptor de
24	39	45.9	156	2 C82971	conserved hypothet
25	39	45.9	161	2 S04917	T-cell receptor de
26	39	45.9	166	2 S04934	T-cell receptor de
27	39	45.9	295	2 A37412	T-cell receptor de
28	39	45.9	336	2 S09532	int protein - phag
29	39	45.9	514	2 E86738	multidrug resistan

30	39	45.9	666	2 I58169	semaphorin III - m
31	39	45.9	771	2 D49423	semaphorin III pre
32	39	45.9	772	2 A49069	collapsin - chicke
33	39	45.9	772	2 I48747	semaphorin D - mou
34	38	44.7	393	2 T03313	gene 16 protein -
35	38	44.7	410	1 O4BS6M	cytochrome P450 10
36	38	44.7	437	2 A34800	Opaque-2 protein -
37	38	44.7	460	2 S06022	regulatory protein
38	38	44.7	527	2 S15089	glucuronosyltransf
39	38	44.7	528	2 JN0619	glucuronosyltransf
40	38	44.7	529	2 A42233	glucuronosyltransf
41	38	44.7	533	1 QRECM2	methyl-accepting c
42	38	44.7	533	2 C90953	methyl-accepting c
43	38	44.7	533	2 G85801	serine chemorecept
44	38	44.7	551	1 GRECS	methyl-accepting c
45	38	44.7	554	2 C91293	methyl-accepting c

ALIGNMENTS

RESULT 1

A58458  
isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces cattleya  
C;Species: Streptomyces.cattleya  
C;Date: 30-Sep-1993 #sequence\_revision 21-Jan-1997 #text\_change 09-Jul-2004  
C;Accession: A58458  
R;Wang, Y.G.; Li, R.F.  
Acta Microbiol. Sin. 36, 87-92, 1996  
A;Title: Cloning and sequencing the isopenicillin N synthetase (IPNS) gene from Streptom  
A;Reference number: A58458  
A;Accession: A58458  
A;Molecule type: DNA  
A;Residues: 1-321 <WAN>  
A;Cross-references: UNIPROT:Q53932; UNIPARC:UPI000012D7FD  
C;Superfamily: isopenicillin N synthase  
C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase  
F;49,213,269/Binding site: iron (His) #status predicted

Query Match 52.9%; Score 45; DB 2; Length 321;  
Best Local Similarity 50.0%; Pred. No. 3.4;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPVTEQQATTW 15

Db 61 NESTTMTDQRSTTW 74

RESULT 2

JC5171

D-galactose-binding periplasmic protein mglB-2 - syphilis spirochete  
N;Alternate names: carbohydrate receptor; methylgalactoside transport galactose-binding  
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C;Date: 16-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: JC5171; D71295  
R;Porcella, S.F.; Popova, T.G.; Hagman, K.E.; Penn, C.W.; Radolf, J.D.; Norgard, M.V.  
Gene 177, 115-121, 1996  
A;Title: A mgl-like operon in Treponema pallidum, the syphilis spirochete.  
A;Reference number: JC5170; MUID:97080510; PMID:8921855  
A;Accession: JC5171  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-403 <POR>  
A;Cross-references: UNIPROT:Q08255; UNIPARC:UPI000012F062; GB:IU48416; NID:G1230600; PIDN  
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
rson, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDO  
Science 281, 375-388, 1998  
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A;Reference number: A71250; MUID:98332770; PMID:9665876  
A;Accession: D71295

A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA

A;Residues: 1-403 <COL>  
A;Cross-references: UNIPARC:UPI000012F062; GB:AE001242; GB:AE000520; NID:G3322976; PIDN:  
A;Experimental source: strain Nichols  
C;Comment: This protein is a component of an ATP-binding cassette operon involved in gal  
C;Genetics:  
A;Gene: mgIB; TP0684  
C;Keywords: calcium binding; chemotaxis; periplasmic space; sugar transport  
F;44,114,116,120,197,220/Binding site: galactose (Asn, His, Asp, Arg, Asn, Asp) #status  
F;96,98,100,102,104,191/Binding site: calcium (Asp, Asn, Asp, Ile, Gly, Asp) #status pre

Query Match 51.2%; Score 43.5; DB 2; Length 403;  
Best Local Similarity 55.6%; Pred. No. 8.1;  
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 HNDSPVRTE---QQATTW 15  
||||| : ||  
Db 114 HNDSKVRTEGIRALGTW 131

RESULT 3  
S58484  
gag protein - maize  
C;Species: Zea mays (maize)  
C;Date: 29-Nov-1985 #sequence\_revision 01-Mar-1996 #text\_change 29-Oct-1999  
C;Accession: S58484  
R;Hu, W.; Das, O.P.; Messing, J.  
Mol. Gen. Genet. 248, 471-480, 1995  
A;Title: Zeon-1, a member of a new maize retrotransposon family.  
A;Reference number: S58484; MUID:96004768; PMID:7565611  
A;Accession: S58484  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-375 <HNU>  
A;Cross-references: UNIPARC:UPI000011DE94; EMBL:U11059; NID:G507844; PIDN:AAA93147.1; PI  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

Query Match 50.6%; Score 43; DB 2; Length 375;  
Best Local Similarity 66.7%; Pred. No. 9.2;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 SPVRTEQQATTW 15  
|||:|||||  
Db 61 SPLSTELQATPW 72

RESULT 4  
D87485  
glutamyI-tRNA synthetase [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: D87485  
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: D87485  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-470 <STO>  
A;Cross-references: UNIPROT:Q9A721; UNIPARC:UPI00000C7547; GB:AE005673; NID:gl3423356; E  
C;Genetics:  
A;Gene: CC1905  
C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

Query Match 50.6%; Score 43; DB 2; Length 470;  
Best Local Similarity 46.7%; Pred. No. 12;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15  
|||:|||||  
Db 274 HGDDVEVFTDEQAISW 288

## RESULT 5

AF2006  
hypothetical protein alr1604 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AF2006  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AF2006  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-247 <KUR>  
A;Cross-references: UNIPROT:Q8YWK9; UNIPARC:UPI00000CE143; GB:BA000019; PIDN:BA877970.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr1604

Query Match 49.4%; Score 42; DB 2; Length 247;  
Best Local Similarity 33.3%; Pred. No. 8.8;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15  
|::|:|:|  
Db 13 HREAPIEVERMGLTW 27

## RESULT 6

E49348  
succinoglycan biosynthesis glycosyltransferase (EC 2.4.1.-) exow [validated] - Rhizobium  
C;Species: Rhizobium meliloti  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: E49348  
R;Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.  
J. Bacteriol. 175, 7033-7044, 1993  
A;Title: Family of glycosyl transferases needed for the synthesis of succinoglycan by Rh  
A;Reference number: A49348; MUID:94042869; PMID:8226645  
A;Accession: E49348  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-283 <GLU>  
A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000016FEBF; GB:L20758; NID:G393240; PIDN:  
C;Genetics:  
A;Gene: exow  
C;Function:

A;Description: EC 2.4.1.-; succinoglycan biosynthesis glycosyltransferase [validated, MU  
, exoU, and exow together are responsible for sugar addition to the lipid carrier  
A;Pathway: succinoglycan biosynthesis  
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 283;  
Best Local Similarity 57.1%; Pred. No. 10;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSPVRTTEQQATTW 15  
|||||:|:|  
Db 232 NDSQFLKQENTW 245

## RESULT 7

A95976  
glucosyltransferase protein (EC 2.4.1.-) [imported] - Sinorhizobium meliloti (strain 102  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: A95976  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: A95976  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-319 <KUR>  
A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000012A384; GB:AL591985; PIDN:CAC49473.1;  
A;Experimental sources: strain 1021, megaplaamid pSymb  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Charn, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholt, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
C;Contents: annotation  
C;Genetics:  
A;Gene: exoW; Smb21690  
A;Genome: plasmid  
C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase  
C;Keywords: Glycosyltransferase; hexosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSFVRTEQQATTW 15  
||||| :|||  
Db 232 NDSFQFLKQGFNTW 245

RESULT 8  
S40175  
ExoW protein - Rhizobium meliloti  
C;Species: Rhizobium meliloti  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S40175  
R;Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A.  
submitted to the EMBL Data Library, April 1993  
A;Description: Analysis of the Rhizobium meliloti genes exoU, exoV, exoW, exoT and exoI ses.

A;Reference number: S40173  
A;Accession: S40175  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-319 <BEC>  
A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000012A384; EMBL:Z22646; NID:G605659; PID  
C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSFVRTEQQATTW 15  
||||| :|||  
Db 232 NDSFQFLKQGFNTW 245

RESULT 9  
B97851  
hypothetical protein RC1210 [imported] - Rickettsia conorii (strain Malish 7)  
C;Species: Rickettsia conorii  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: B97851  
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rickettsia conorii  
Science 293, 2093-2098, 2001  
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A;Reference number: A97700; MUID:21442074; PMID:11557893  
A;Accession: B97851  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-101 <KUR>  
A;Cross-references: UNIPROT:Q92GB3; UNIPARC:UPI000000CC02C; GB:AE006914; PIDN:AAL03748.1;

C;Genetics:  
A;Gene: RC1210

Query Match 48.2%; Score 41; DB 2; Length 101;  
Best Local Similarity 60.0%; Pred. No. 4.9;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQ 10  
||||| :|||  
Db 41 HNDDPISTQQ 50

RESULT 10  
B85066  
hypothetical protein AT4g05260 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B85066  
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; MUID:20083488; PMID:10617198  
A;Accession: B85066  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-259 <STO>  
A;Cross-references: UNIPROT:Q9M0W9; UNIPARC:UPI000000A640D; GB:NC\_001268; NID:G7267286; P  
C;Genetics:  
A;Gene: AT4g05260  
A;Map position: 4

Query Match 48.2%; Score 41; DB 2; Length 259;  
Best Local Similarity 63.6%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQ 11  
||||| :|||  
Db 140 HQDSPVRNNEQ 150

RESULT 11  
T20181  
hypothetical protein C53B4.4c - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Dec-2004  
C;Accession: T20181  
R;Barks, M.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: Z19233  
A;Accession: T20181  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1449 <WIL>  
A;Cross-references: UNIPROT:Q9U3L2; UNIPARC:UPI00001641A7; EMBL:Z68215; PIDN:CABS4213.1;  
A;Experimental source: clone C53B4  
C;Genetics:  
A;Gene: CESP:C53B4.4c  
A;Map position: 4  
A;Introns: 15/3; 92/2; 252/3; 306/1; 477/2; 571/1; 605/1; 720/3; 880/3; 1008/2; 1091/1;

Query Match 48.2%; Score 41; DB 2; Length 1449;  
Best Local Similarity 58.3%; Pred. No. 92;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NDSFVRTEQQAT 13  
||||| :|||  
Db 423 NNVPFIRSQAT 434

RESULT 12  
T20180  
hypothetical protein C53B4.4a - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans





GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 58.4848 Seconds  
(without alignments)  
237.245 Million cell updates/sec

Title: US-10-758-165a-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	50	58.8	397	2	Q6Q4A6 TETTH
2	50	58.8	1522	2	Q5CQB3 CRYPV
3	48	56.5	735	2	Q8XXG1 RALSO
4	47	55.3	84	2	Q7PCB5 GOSAR
5	47	55.3	1083	2	Q94189 CRYNE
6	47	55.3	2360	2	Q94188 CRYNE
7	47	55.3	2360	2	Q55R83 CRYNE
8	47	55.3	2360	2	Q5K8V7 CRYNE
9	46	54.1	425	2	Q9VG94 DROME
10	46	54.1	446	2	Q3ZAP4 DROME
11	46	54.1	449	2	Q8MTZ6 DROME
12	46	54.1	526	2	Q8AWF6 DROME
13	46	54.1	621	2	Q9VG85 DROME
14	45.5	53.5	700	2	Q8SQK3 ENCCU
15	45	52.9	79	2	Q4KE23 PSE14
16	45	52.9	296	2	Q3KEF4 PSEPF
17	45	52.9	321	1	IPNS_STRCT
18	45	52.9	407	2	Q4WH60 ASPFU
19	44	51.8	673	2	Q4HW10 DROME
20	43.5	51.2	403	1	MLGB_TREPA
21	43	50.6	362	2	Q2SBJ8 GAGMM
22	43	50.6	470	1	SYE_CAUCR
23	43	50.6	521	2	Q3W9L5 ACTO
24	43	50.6	774	2	Q8J1W9 XENLA
25	43	50.6	832	2	Q5E2F3 VIBF1
26	43	50.6	1378	2	Q4PFK4 USTWA
27	43	50.6	2742	2	Q8XX21 RALSO
28	43	50.6	2742	2	Q4SZV7 TETNG
29	42	49.4	79	2	Q4ZNL8 PSEU2
30	42	49.4	79	2	Q87WK0 PSESM
31	42	49.4	194	2	Q67J75 SYMBH

32	42	49.4	221	2	Q7PK01 ANOGA
33	42	49.4	228	2	Q4E2I5 TRYCR
34	42	49.4	247	2	Q8YWK9 ANASP
35	42	49.4	260	2	Q73S26 MYCPA
36	42	49.4	262	2	Q7XBD0 MAIZE
37	42	49.4	296	1	ZN75A HUMAN
38	42	49.4	319	1	EXOM_RHIME
39	42	49.4	326	2	Q6C666 YARLI
40	42	49.4	403	2	Q7Q1A0 ANOGA
41	42	49.4	646	2	Q6BGK5 PARTE
42	42	49.4	732	2	Q6LNO6 PHOPR
43	42	49.4	817	2	Q6ZPN1 MOUSE
44	42	49.4	983	2	Q4PR6 USTWA
45	42	49.4	983	2	Q96VE8 USTWA

ALIGNMENTS

RESULT 1  
ID Q6Q4A6 TETTH PRELIMINARY; PRT; 397 AA.  
AC Q6Q4A6;  
DT 05-JUL-2004, integrated into UniProtKB/TREMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE Mitogen activated protein kinase 4.  
OS Tetrahymena thermophila.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
OC Tetrahymenina; Tetrahymenidae; Tetrahymena.  
ON NCBI\_TaxID=5911;  
RN NUCLEOTIDE SEQUENCE.  
RP Arslanyolu M., Yildiz M.T.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC EMBL; AY560586; AAS55115.1; -; Genomic\_DNA.  
DR HSSP; P24941; 1KE8.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0000166; F:nucleotide binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR003521; MAP\_kin.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS01351; MAPK; UNKNOWN 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-Binding.  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 397 AA; 45764 MW; 43AEE281F714E071 CRC64;

Query Match 58.8%; Score 50; DB 2; Length 397;  
Best Local Similarity 64.3%; Pred.No.5.9; Mismatches 2; Indels 0; Gaps 0;  
Matches 9; Conservative 3;

Qv 2 NDSFVTEQQATTW 15  
:|||||  
Db 169 DDNPVTEYVATRW 182

RESULT 2

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O5CQB3 CRYPV
ID O5CQB3 CRYPV PRELIMINARY; PRT; 1522 AA.
AC O5CQB3;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Possible ABC transporter with AAA domain and 12 transmembrane domains.
GN ORFNames=cgd4_1190;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
RA Lanto C.A., Deng M., Liu C., Widmer G., Tripori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum."
RL Science 304:441-445(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDAJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAER01000009; EAK87614.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
KW SEQUENCE 1522 AA; 176017 MW; 75C04515093B3981 CRC64;
SQ
Query Match 58.8%; Score 50; DB 2; Length 1522;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15
||| ||| :|||
Db 72 HNDKQVPESEISTW 86

RESULT 3
ID Q8XXG1 RALSO PRELIMINARY; PRT; 735 AA.
AC Q8XXG1;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE PROBABLE BIFUNCTIONAL ENZYME : (P)PGPP SYNTHETASE II AND GUANOSINE-
DE 3',5'-BISDIPHOSPHATE 3'-PYROPHOSPHOHYDROLASE (PPGPPASE) PROTEIN
DE (EC 2.7.6.5) (EC 3.1.7.2).
GN Name=spot; OrderedLocusNames=RSC2153; ORFNames=RS01611;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangerot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,

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RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502(2002).
CC -!- FUNCTION: In eubacteria ppGpp (guanosine 3'-diphosphate 5'-
CC diphosphate) is a mediator of the stringent response that
CC coordinates a variety of cellular activities in response to
CC changes in nutritional abundance. This enzyme catalyzes the
CC formation of ppGpp which is then hydrolyzed to form ppGpp (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + GTP = AMP + guanosine 3'-diphosphate 5'-
CC triphosphate.
CC -!- PATHWAY: ppGpp metabolism; first step.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AL646068; CAD15860.1; -; Genomic DNA.
DR BioCyc; RSO1305; RSC2153-MONOMER; -.
DR GO; GO:0016597; F:amino acid binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0008893; F:guanosine-3',5'-bis(diphosphate) 3'-diphosph. .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0015969; P:guanosine tetraphosphate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002912; ACT_bd.
DR InterPro; IPR012675; Ferredoxin_fold.
DR InterPro; IPR006674; HD_hydro.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR007685; RelA_Spot.
DR InterPro; IPR004811; Spot_rela.
DR InterPro; IPR004095; TGS.
DR InterPro; IPR012676; TGS-like.
DR Pfam; PF01842; ACT; 1.
DR Pfam; PF01966; HD; 1.
DR Pfam; PF04607; RelA_Spot; 1.
DR Pfam; PF02824; TGS; 1.
DR SMART; SM00471; Hdc; 1.
DR TIGRFAMs; TIGR00691; spot_rela; 1.
DR Complete proteome; Hydrolase; Kinase; Transferase.
KW SEQUENCE 735 AA; 81962 MW; 9A6B0054104FD241 CRC64;
SQ
Query Match 56.5%; Score 48; DB 2; Length 735;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15
||| ||| :|||
Db 358 HHDEPDRAQQQAQHW 372

RESULT 4
Q7PCB5 GOSAR
ID Q7PCB5 GOSAR PRELIMINARY; PRT; 84 AA.
AC Q7PCB5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Putative phytylsulfokine peptide precursor.
GN Name=PSK1;
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=29729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=
RX
RA Lorbiecke R., Sauter M.M.;
RA "Comparative analysis of PSK peptide growth factor precursor

```

```
RT homologs."
RL Plant Sci. 163:321-332 (2002).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ third party annotation (TPA) entry.
CC -----
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CC -----
DR ENBL; BK000114; DAA00278.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR InterPro; IPR009438; PSK.
DR Pfam; PF06404; PSK; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 84 AA; 9242 MW; 6B04F8D05EC36C9B CRC64;

Query Match 55.3%; Score 47; DB 2; Length 84;
Best Local Similarity 61.5%; Pred. No. 3.6; Indels 3; Mismatches 2; Gaps 0;
Matches 8; Conservative 2;

QY 2 NDSPVRTEQQATT 14
Db ||||| :|: |||
32 NDSFATQSQGTT 44

RESULT 5
O94189 CRYNE PRELIMINARY; PRT; 1083 AA.
AC O94189 CRYNE PRELIMINARY; PRT; 1083 AA.
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Phosphatidylinositol 3-kinase TOR1 (Fragment).
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B3501; PubMed=10330150;
RX MEDLINE=99262981; Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heitman J.;
RA "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112 (1999).
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CC -----
DR ENBL; AF098973; AAD16274.1; -; mRNA.
DR HSP; P42345; IAU.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR004003; PI3/4_kinase_cat.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02260; FATC; 1.
DR SMART; SM00146; PI3KC; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS0290; PI3_4_KINASE_3; 1.
KW Kinase; Transferase.
FT NON_TER 1083 1083
SQ SEQUENCE 1083 AA; 123973 MW; 0C48A17D75853A9 CRC64;
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```
Query Match 55.3%; Score 47; DB 2; Length 1083;
Best Local Similarity 53.3%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATT 15
Db ||||| :|: |||
202 HADEPARQEMQRTW 216

RESULT 6
O94188 CRYNE PRELIMINARY; PRT; 2360 AA.
AC O94188 CRYNE PRELIMINARY; PRT; 2360 AA.
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Phosphatidylinositol 3-kinase TOR1.
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H99; PubMed=10330150;
RX MEDLINE=99262981; Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heitman J.;
RA "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112 (1999).
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DR ENBL; AF098972; AAD16273.1; -; Genomic_DNA.
DR HSP; P42345; IAU.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity; IEA.
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DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR000357; HEAT.
DR InterPro; IPR004003; PI3/4_kinase_cat.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR SMART; SM00146; PI3KC; 1.
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DR PROSITE; PS0290; PI3_4_KINASE_3; 1.
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1479 HADEPARQEMQRTW 1493

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DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
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DE Hypothetical protein.  
GN ORFNames=CNBF1080;  
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OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
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RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B-3501A;  
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
RA Wickes B.L., Fu J., Davis R.W.;  
RL "Cryptococcus neoformans serotype D sequencing";  
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC EMBL; AA00100030; EAL20296.1; -; Genomic\_DNA.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . ; IEA.  
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DR InterPro; IPR000403; PI3/4\_kinase\_cat.  
DR InterPro; IPR011990; TPR-like\_helical.  
DR Pfam; PF02259; FAT; 1.  
DR Pfam; PF02260; FATC; 1.  
DR Pfam; PF02985; HEAT; 3.  
DR Pfam; PF00454; PI3\_P14\_kinase; 1.  
DR SMART; SM00146; PI3KC; 1.  
DR PROSITE; PS00915; PI3\_4\_KINASE\_1; 1.  
DR PROSITE; PS02090; PI3\_4\_KINASE\_3; 1.  
KW Hypothetical protein.  
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DT 07-FEB-2006, entry version 9.  
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OX NCBI\_TaxID=5207;  
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=JEC21.  
RX PubMed=15653466; DOI=10.1126/science.1103773;  
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
RA Mathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
RA D'Souza C.A., Fox D.S., Gruberg V., Fu J., Fukushima M., Haas B.J.,  
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzyzinski M.I.,  
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,  
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggall F.R., Salzberg S.L.,  
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
RA Fraser C.M., Hyman R.W.;

RT "The genome of the basidiomycetous yeast and human pathogen  
RT Cryptococcus neoformans";  
RL Science 307.1321-1324(2005).  
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CC EMBL; AE017346; AAM44029.1; -; Genomic\_DNA.  
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DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . ; IEA.  
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DR Pfam; PF02260; FATC; 1.  
DR Pfam; PF02985; HEAT; 3.  
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DR PROSITE; PS02090; PI3\_4\_KINASE\_3; 1.  
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DT 01-OCT-2002, sequence version 2.  
DT 07-FEB-2006, entry version 19.  
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OC Ephydroidea; Drosophilidae; Drosophila.  
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RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RX Amaratunga P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RX Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RX Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RX Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RX Abrial J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
RX Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RX Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
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RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RX de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RX Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RX Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RX Fogle C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RX Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RX Harkin N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RX Hostin D., Houston K.F., Howland T.J., Wei M.-H., Ibegwam C.,  
RX Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Furi V., Reese M.G.,  
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou Q., Zheng L.,  
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195 (2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT *melanogaster* euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genome perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RG Berkeley *Drosophila* Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "*Drosophila melanogaster* release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RG FlyBase;  
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; AE003690; AAF54601.2; -; Genomic\_DNA.  
DR FlyBase; FBgn037872; nocturnin.  
DR InterPro; IPR005135; Exo\_endo\_phos.  
DR Pfam; PF03372; Exo\_endo\_phos; 1.  
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DB 109 HNDGFVRCPEALTW 123  
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DT 27-SEP-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE R565127P.  
GN Names=nocturnin;  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
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OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
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RC STRAIN=Berkley;  
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,  
RA Park S., Wan K., Yu C., Celniker S.;  
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; BT023825; AA286746.1; -; mRNA.  
DR InterPro; IPR005135; Exo\_endo\_phos.  
DR Pfam; PF03372; Exo\_endo\_phos; 1.  
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Best Local Similarity 53.3%; Pred. No. 34;  
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DB 130 HNDGFVRCPEALTW 144  
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DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
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OC Ephydroidea; Drosophilidae; Drosophila.  
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RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22730715; PubMed=11747467;  
RA Dupressoir A., Morel A.-P., Barbot W., Loireau M.-P., Corbo L.,  
RA Heidmann T.;  
RT "Identification of four families of yCCR4- and Mg2+-dependent  
RT endonuclease-related proteins in higher eukaryotes, and  
RT characterization of orthologs of yCCR4 with a conserved leucine-rich  
RT repeat essential for hCAFI/hPOP2 binding.";  
RT BMC Genomics 2:9-9(2001).  
CC



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[5]
RN NUCLEOTIDE SEQUENCE.
RP Berkeley Drosophila Genome Project;
RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirekas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AE003690; AAF54600.2; -; Genomic_DNA.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
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Db 305 HNDGFVRCPEALTW 319

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DT 07-FEB-2006, entry version 18.
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OS Encephalitozoon cuniculi
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=GB-M1;
MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
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DR EMBL; AL590451; CAD27151.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
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DR GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. . ; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR000711; ATPsyn_OSCP.
DR InterPro; IPR002355; Cu oxidase Cu BS.
DR InterPro; IPR002490; V_ATPase_sub116.
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DR Pfam; PF01496; V_ATPase_i; 1.
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DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
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OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=264730;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
RA Crabtree J., Creasy T., Daviden T.M., Haft D.H., Zafar N., Zhou L.,
RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,
RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,
RA Mansfield J., Collmer A., Buell R.;
RT "Whole-genome sequence analysis of Pseudomonas syringae pv.
RT phaseolicola 1448A reveals divergence among pathogens in genes
RT involved in virulence and transposition.";
RL J. Bacteriol. 187:6488-6498(2005).
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DR EMBL; CP000058; AAZ36295.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 79 AA; 8809 MW; D167EB243339F201 CRC64;

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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 14.8485 Seconds  
(without alignments)  
88.424 Million cell updates/sec

Title: US-10-758-165a-2

Perfect score: 85

Sequence: 1 HNDSPVTEQQATW 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/iaa/PTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	431	2	US-09-479-614-14
2	85	100.0	496	2	US-09-479-614-2
3	85	100.0	496	2	US-09-479-614-29
4	48	56.5	108	2	US-09-281-760E-37
5	48	56.5	312	2	US-09-701-623C-2
6	48	56.5	426	1	US-08-336-583-2
7	48	56.5	426	5	PCT-US95-13795-2
8	46	54.1	210	2	US-09-270-767-45299
9	45	52.9	321	2	US-09-413-231-8
10	45	52.9	321	3	US-09-924-841-8
11	44	51.8	181	2	US-09-270-767-43758
12	42	49.4	178	2	US-10-104-047-3886
13	42	49.4	296	2	US-10-094-749-2367
14	41	48.2	381	2	US-09-605-703B-1364
15	41	48.2	534	2	US-09-605-703B-1362
16	40	47.1	540	2	US-09-949-016-8465
17	40	47.1	540	2	US-09-949-016-9052
18	39	45.9	225	2	US-09-252-991A-17094
19	39	45.9	655	2	US-08-556-422A-3
20	39	45.9	771	1	US-08-121-713D-54
21	39	45.9	771	1	US-08-835-268-54
22	39	45.9	771	1	US-09-060-692-54
23	39	45.9	771	2	US-08-833-391-54
24	39	45.9	771	2	US-09-060-610-54
25	39	45.9	771	5	PCT-US94-10151A-54
26	38	44.7	127	2	US-09-270-767-39006

#### ALIGNMENTS

##### RESULT 1

US-09-479-614-14

; Sequence 14, Application US/09479614

; Patent No. 6573372

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; CURRENT FILING DATE: 2000-01-07

; EARLIER APPLICATION NUMBER: 60/115,033

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 431

; TYPE: PRT

; ORGANISM: Felis catus

; ORGANISM: Felis catus

; US-09-479-614-14

Query Match 100.0%; Score 85; DB 2; Length 431;

Best Local Similarity 100.0%; Pred. No. 1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATW 15

Db 362 HNDSPVTEQQATW 376

##### RESULT 2

US-09-479-614-2

; Sequence 2, Application US/09479614

; Patent No. 6573372

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; CURRENT FILING DATE: 2000-01-07

; EARLIER APPLICATION NUMBER: 60/115,033

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 496

; TYPE: PRT

; ORGANISM: Felis catus

; ORGANISM: Felis catus

Sequence 54223, A  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 50, Appl  
Sequence 52, Appl  
Sequence 8, Appli  
Sequence 6999, Ap  
Sequence 2, Appli  
Sequence 5, Appli  
Sequence 11880, A  
Sequence 5612, Ap  
Sequence 6291, Ap  
Sequence 25916, A  
Sequence 2576, Ap  
Sequence 1193, A  
Sequence 8156, Ap  
Sequence 15717, A  
Sequence 4442, Ap  
Sequence 306, App

27 38 44.7 127 2 US-09-270-767-54223  
28 38 44.7 449 2 US-09-784-340-4  
29 38 44.7 527 2 US-09-784-340-2  
30 38 44.7 527 3 US-10-114-270-50  
31 38 44.7 527 3 US-10-114-270-52  
32 38 44.7 528 2 US-09-356-806-8  
33 38 44.7 528 2 US-09-949-016-6999  
34 38 44.7 530 2 US-09-180-852-2  
35 38 44.7 530 2 US-09-784-340-5  
36 38 44.7 649 2 US-09-489-039A-11880  
37 38 44.7 704 2 US-09-107-532A-5612  
38 44.7 1092 2 US-09-134-000C-6291  
39 37.5 44.1 447 2 US-09-252-991A-25916  
40 37.5 44.1 1124 2 US-09-605-703B-2576  
41 37 43.5 113 2 US-09-902-540-11193  
42 37 43.5 116 2 US-09-513-999C-8156  
43 37 43.5 236 2 US-09-248-796A-15717  
44 37 43.5 249 2 US-09-134-001C-4442  
45 37 43.5 249 2 US-09-710-279-306

US-09-479-614-2

Query Match 100.0%; Score 85; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15  
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Db 427 HNDSPVRTEQQATTW 441

RESULT 3

US-09-479-614-29  
; Sequence 29, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; EARLIER FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-29

Query Match 100.0%; Score 85; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15  
|||||  
Db 427 HNDSPVRTEQQATTW 441

RESULT 4

US-09-281-760E-37  
; Sequence 37, Application US/09281760E  
; Patent No. 6734287  
; GENERAL INFORMATION:  
; APPLICANT: Lawton, Robert  
; APPLICANT: Mermer, Brion  
; APPLICANT: Francoeur, Greg  
; TITLE OF INVENTION: Specific Binding Protein for Treating  
; TITLE OF INVENTION: Canine Allergy  
; FILE REFERENCE: 01-1275A  
; CURRENT APPLICATION NUMBER: US/09/281,760E  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: 09/058,331  
; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (136)..(136)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (413)..(414)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (451)..(451)

; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (460)..(462)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (500)..(500)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (530)..(530)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (568)..(568)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (847)..(849)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (853)..(853)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1382)..(1382)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1832)..(1832)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
US-09-281-760E-37

Query Match 56.5%; Score 48; DB 2; Length 108;  
Best Local Similarity 61.5%; Pred. No. 0.65;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14  
|||||  
Db 44 NDSPIQTQYTTT 56

RESULT 5

US-09-701-623C-2  
; Sequence 2, Application US/09701623C  
; Patent No. 6811782  
; GENERAL INFORMATION:  
; APPLICANT: Wang Ph.D., Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; TITLE OF INVENTION: ALLERGY  
; FILE REFERENCE: 11514153US1  
; CURRENT APPLICATION NUMBER: US/09/701,623C  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Dog  
; FEATURE:  
; OTHER INFORMATION: CH2CH3n of dog IgE  
; PUBLICATION INFORMATION:  
; AUTHORS: Patel,  
; JOURNAL: Immunogenetics  
; VOLUME: 41  
; PAGES: 282-286  
; DATE: 1995

## US-09-701-623C-2

Query Match 56.5%; Score 48; DB 2; Length 312;  
Best Local Similarity 61.5%; Pred. No. 2.1;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVRTEQQATT 14  
||||:|:|  
Db 256 NDSPIQTDQVTTT 268

## RESULT 6

US-08-336-583-2  
; Sequence 2, Application US/08336583  
; Patent No. 5629415  
; GENERAL INFORMATION:  
; APPLICANT: HOLLIS, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/336,583  
; FILING DATE: 09-NOV-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E.  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19211  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-6734  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-13795-2

Query Match 56.5%; Score 48; DB 1; Length 426;  
Best Local Similarity 61.5%; Pred. No. 3;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVRTEQQATT 14  
||||:|:|  
Db 358 NDSPIQTDQVTTT 370

## RESULT 7

PCT-US95-13795-2  
; Sequence 2, Application PC/TUS9513795  
; GENERAL INFORMATION:  
; APPLICANT: HOLLIS, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000  
; CITY: RAHWAY

Query Match 56.5%; Score 48; DB 1; Length 426;  
Best Local Similarity 61.5%; Pred. No. 3;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVRTEQQATT 14  
||||:|:|  
Db 358 NDSPIQTDQVTTT 370

## RESULT 8

US-09-270-767-45299  
; Sequence 45299, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 45299  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; US-09-270-767-45299

Query Match 54.1%; Score 46; DB 2; Length 210;  
Best Local Similarity 53.3%; Pred. No. 3.1;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATTW 15  
||||:|:|  
Db 149 HNDGFVRCPEALTW 163

STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13795  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CARTY, CHRISTINE E.  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 19211  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-6734  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-13795-2

Query Match 56.5%; Score 48; DB 5; Length 426;  
Best Local Similarity 61.5%; Pred. No. 3;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVRTEQQATT 14  
||||:|:|  
Db 358 NDSPIQTDQVTTT 370

## RESULT 9

US-09-413-231-8  
; Sequence 8, Application US/09413231  
; Patent No. 6284483  
; GENERAL INFORMATION:  
; APPLICANT: Dilley, David R.  
; APPLICANT: Kadyrzhanova, Dina K  
; APPLICANT: Wang, Zhenyong  
; APPLICANT: Warner, Toni M

Query Match 54.1%; Score 46; DB 2; Length 210;  
Best Local Similarity 53.3%; Pred. No. 3.1;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATTW 15  
||||:|:|  
Db 149 HNDGFVRCPEALTW 163

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; TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
; TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
; FILE REFERENCE: MSU41-453
; CURRENT APPLICATION NUMBER: US/09/413,231
; CURRENT FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified IPNV
; OTHER INFORMATION: from Streptomyces cattleya
; NAME/KEY: MUTAGEN
; LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNV modified to Arg
; US-09-413-231-8

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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43758
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43758

Query Match          51.8%; Score 44; DB 2; Length 181;
Best Local Similarity 57.1%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2  NDSPVRTEQQATTW 15
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Db       62  NCSPIQIEVQAIQW 75

RESULT 12
US-10-104-047-3886
; Sequence 3886, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3886
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3886

Query Match          49.4%; Score 42; DB 2; Length 178;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1  HNDSPVRTEQQATTW 15
        |  ||:|||||
Db       8  HQDPFVKRKKLSTW 22

RESULT 13
US-10-094-749-2367
; Sequence 2367, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SERI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOUKI

```

```
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2367
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2367

Query Match 49.4%; Score 42; DB 2; Length 296;
Best Local Similarity 40.0%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATW 15
Db 126 HQDFPVKKKLSIW 140
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RESULT 14
US-09-605-703B-1364
; Sequence 1364, Application US/09605703B
; Patent No. 8962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1364
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1364

Query Match 48.2%; Score 41; DB 2; Length 381;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATW 15
Db 185 HSDKPIRHEAEKLGW 199
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RESULT 15
US-09-605-703B-1362
; Sequence 1362, Application US/09605703B
; Patent No. 8962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
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; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1362
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1362

Query Match 48.2%; Score 41; DB 2; Length 534;
Best Local Similarity 40.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Db 185 HSDKPIRHEAEKLGW 199
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Job time : 15.8485 secs
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 75.7576 Seconds  
(without alignments)  
91.717 Million cell updates/sec

Title: US-10-758-165a-2

Perfect score: 85

Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	5	US-10-758-165-2
2	85	100.0	431	3	US-09-479-614-14
3	85	100.0	431	4	US-10-409-772-14
4	85	100.0	496	3	US-09-479-614-2
5	85	100.0	496	3	US-09-479-614-29
6	85	100.0	496	4	US-10-214-524-25
7	85	100.0	496	4	US-10-409-772-2
8	85	100.0	496	4	US-10-409-772-29
9	48	56.5	15	5	US-10-758-165-1
10	48	56.5	312	5	US-10-723-207-2
11	48	56.5	426	4	US-10-214-524-28
12	47	55.3	68	4	US-10-425-115-203123
13	47	55.3	84	5	US-10-474-691-101
14	47	55.3	1083	5	US-10-732-923-13976
15	47	55.3	2360	5	US-10-732-923-13960
16	46	54.1	449	6	US-11-097-143-9714
17	45	52.9	321	3	US-09-924-841-8
18	44	51.8	194	4	US-10-437-963-145550
19	44	51.8	673	6	US-11-097-143-42006
20	43	50.6	151	4	US-10-425-115-283053
21	43	50.6	425	4	US-10-425-115-190849
22	43	50.6	433	4	US-10-425-115-189170
23	43	50.6	435	4	US-10-425-115-320857
24	43	50.6	459	4	US-10-425-115-184927
25	43	50.6	461	4	US-10-425-115-320858
26	43	50.6	470	4	US-10-369-493-16930
27	43	50.6	493	4	US-10-425-115-190842

28	43	50.6	503	4	US-10-425-115-351700	Sequence 351700,
29	43	50.6	505	4	US-10-425-115-184928	Sequence 184928,
30	43	50.6	505	4	US-10-425-115-189173	Sequence 189173, A
31	43	50.6	696	4	US-10-425-114-38018	Sequence 38018, A
32	43	50.6	716	4	US-10-425-115-336115	Sequence 336115,
33	42.5	50.0	188	4	US-10-437-963-201785	Sequence 201785,
34	42	49.4	68	4	US-10-425-115-233639	Sequence 233639,
35	42	49.4	178	4	US-10-104-047-3886	Sequence 3886, Ap
36	42	49.4	178	6	US-11-072-512-3886	Sequence 3886, Ap
37	42	49.4	197	4	US-10-029-386-34079	Sequence 34079, A
38	42	49.4	262	4	US-10-425-115-220304	Sequence 220304,
39	42	49.4	296	4	US-10-094-749-23367	Sequence 23367, Ap
40	42	49.4	537	4	US-10-479-435-15	Sequence 15, Appl
41	41	48.2	152	3	US-09-864-761-37742	Sequence 37742, A
42	41	48.2	473	4	US-10-424-599-153291	Sequence 153291,
43	41	48.2	647	3	US-09-738-626-6449	Sequence 6449, Ap
44	41	48.2	671	4	US-10-767-701-45175	Sequence 45175, A
45	41	48.2	750	5	US-10-732-923-11093	Sequence 11093, A

ALIGNMENTS

RESULT 1

US-10-758-165-2

; Sequence 2, Application US/10758165

; Publication No. US20050196816A1

; GENERAL INFORMATION:

; APPLICANT: Hammerberg, Bruce

; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

; FILE REFERENCE: 5051-661

; CURRENT APPLICATION NUMBER: US/10758,165

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: US 60/440,472

; PRIOR FILING DATE: 2003-01-16

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Felis catus

US-10-758-165-2

Query Match 100.0%; Score 85; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15

Db 1 HNDSPVTEQQATTW 15

RESULT 2

US-09-479-614-14

; Sequence 14, Application US/09479614

; Publication No. US20030013183A1

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; CURRENT FILING DATE: 2000-01-07

; EARLIER APPLICATION NUMBER: 60/115,033

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 431

; TYPE: PRT

; ORGANISM: Felis catus

US-09-479-614-14

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Query Match      100.0%; Score 85; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVRTEQQAATTW 15
Db      362 HNDSPVRTEQQAATTW 376

RESULT 3
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match      100.0%; Score 85; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVRTEQQAATTW 15
Db      362 HNDSPVRTEQQAATTW 376

RESULT 4
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match      100.0%; Score 85; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVRTEQQAATTW 15
Db      427 HNDSPVRTEQQAATTW 441

RESULT 5
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
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; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match      100.0%; Score 85; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVRTEQQAATTW 15
Db      427 HNDSPVRTEQQAATTW 441

RESULT 6
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match      100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVRTEQQAATTW 15
Db      427 HNDSPVRTEQQAATTW 441

RESULT 7
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
Query Match      100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  HNDSPVTEQQATTW 15
Db      427 HNDSPVTEQQATTW 441

RESULT 8
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US2003021656A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
Query Match      100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  HNDSPVTEQQATTW 15
Db      427 HNDSPVTEQQATTW 441

RESULT 9
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1
Query Match      56.5%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.25;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2  NDSFVRTEQQATT 14
Db      2  NDSFQTDQYTTT 14

RESULT 10
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2
Query Match      56.5%; Score 48; DB 5; Length 312;
Best Local Similarity 61.5%; Pred. No. 7;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2  NDSFVRTEQQATT 14
Db      256 NDSFQTDQYTTT 268

RESULT 11
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
Query Match      56.5%; Score 48; DB 4; Length 426;
Best Local Similarity 61.5%; Pred. No. 9.9;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2  NDSFVRTEQQATT 14
Db      256 NDSFQTDQYTTT 268
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Db      358 NDSPIQTDQVTTT 370

RESULT 12
US-10-425-115-203123
; Sequence 203123, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 203123
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116836C.1.pep
US-10-425-115-203123

Query Match      55.3%; Score 47; DB 4; Length 68;
Best Local Similarity 69.2%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPIRTEQQATT 14
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Db      38 NQTPVTEQTGTT 50

RESULT 13
US-10-474-691-101
; Sequence 101, Application US/10474691
; Publication No. US20040221332A1
; GENERAL INFORMATION:
; APPLICANT: CropDesign N.V.
; TITLE OF INVENTION: Plant growth regulating genes, proteins and uses thereof
; FILE REFERENCE: CROP-028-PCT
; CURRENT APPLICATION NUMBER: US/10/474,691
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/283,313
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Gossypium arboreum
US-10-474-691-101

Query Match      55.3%; Score 47; DB 5; Length 84;
Best Local Similarity 61.5%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPIRTEQQATT 14
      ||||:|:|
Db      32 NDSPAKTSQGT 44

RESULT 14
US-10-732-923-13976
; Sequence 13976, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13960
; LENGTH: 2360
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. grubii
US-10-732-923-13960

Query Match      55.3%; Score 47; DB 5; Length 2360;
Best Local Similarity 53.3%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 HNDSPIRTEQQATT 15
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Db      1479 HADEPARQEMQRQTW 1493

Search completed: August 30, 2006, 05:13:01
Job time : 76.7576 secs

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13976
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. neoformans
US-10-732-923-13976

Query Match      55.3%; Score 47; DB 5; Length 1083;
Best Local Similarity 53.3%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 HNDSPIRTEQQATT 15
      |||||
Db      202 HADEPARQEMQRQTW 216

RESULT 15
US-10-732-923-13960
; Sequence 13960, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13960
; LENGTH: 2360
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. grubii
US-10-732-923-13960

Query Match      55.3%; Score 47; DB 5; Length 2360;
Best Local Similarity 53.3%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 HNDSPIRTEQQATT 15
      |||||
Db      1479 HADEPARQEMQRQTW 1493

Search completed: August 30, 2006, 05:13:01
Job time : 76.7576 secs
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[illegible]

; SEQ ID NO 7573  
; LENGTH: 174

; TYPE: PRT

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(174)

; OTHER INFORMATION: unsure at all Xaa locations

US-11-330-403-7573

Query Match 44.7%; Score 38; DB 7; Length 174;  
Best Local Similarity 63.6%; Pred. No. 31;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQQA 12

DB 55 NDPPVRNSQEA 65

#### RESULT 8

US-11-330-403-12509  
; Sequence 12509, Application US/11330403

; Publication No. US20060159563A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53629)B

; CURRENT APPLICATION NUMBER: US/11/330,403

; CURRENT FILING DATE: 2006-01-12

; NUMBER OF SEQ ID NOS: 19250

; SEQ ID NO 12509

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(242)

; OTHER INFORMATION: unsure at all Xaa locations

US-11-330-403-12509

Query Match 44.7%; Score 38; DB 7; Length 242;  
Best Local Similarity 63.6%; Pred. No. 43;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQQA 12

DB 144 NDPPVRNSQEA 154

#### RESULT 9

US-10-449-902-37829

; Sequence 37829, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

; FILE REFERENCE: MOA-A020511-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 37829

; LENGTH: 436

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-37829

Query Match 44.7%; Score 38; DB 6; Length 436;  
Best Local Similarity 40.0%; Pred. No. 80;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15

DB 377 HTEAVVENARMATTW 391

#### RESULT 10

US-10-196-749-522

; Sequence 522, Application US/10196749

; Publication No. US20060094864A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C340

; CURRENT APPLICATION NUMBER: US/10/196,749

; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 522

; LENGTH: 527

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-196-749-522

Query Match 44.7%; Score 38; DB 6; Length 527;  
Best Local Similarity 40.0%; Pred. No. 97;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15

DB 447 HHDQPVKPLDRAVFW 461

#### RESULT 11

US-10-700-439-165

; Sequence 165, Application US/10700439

; Publication No. US2006018889A1

; GENERAL INFORMATION:

```

; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Burgess, Christopher
; APPLICANT: Myerow, Susan
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Maimonis, Peter
; APPLICANT: Molino, Gary
; APPLICANT: Burgart, Lawrence
; APPLICANT: Boardman, Lisa A.
; APPLICANT: Thibodeau, Steven
; APPLICANT: Lewis, Marcia
; TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
; FILE REFERENCE: 1657/2022
; CURRENT APPLICATION NUMBER: US/10/700,439
; CURRENT FILING DATE: 2003-11-04
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-439-165

Query Match 44.7%; Score 38; DB 6; Length 530;
Best Local Similarity 40.0%; Pred. No. 98;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15
Db 450 HHDQPVKPLDRAVFW 464

RESULT 12
US-10-519-069-18
; Sequence 18, Application US/10519069
; Publication No. US20060121561A1
; GENERAL INFORMATION:
; APPLICANT: Fritsch Olivier
; APPLICANT: Hohn Barbara
; APPLICANT: Lucht Jan Martin
; TITLE OF INVENTION: GENE FOR INCREASED SOMATIC RECOMBINATION
; FILE REFERENCE: 1-32546B/FMI
; CURRENT APPLICATION NUMBER: US/10/519,069
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/EP03/006757
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: GB 0214896
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-519-069-18

Query Match 44.7%; Score 38; DB 6; Length 596;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PVRTEQQATTW 15
Db 535 PSRTEPQFVTW 545

RESULT 13
US-10-449-902-41297
; Sequence 41297, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National
; APPLICANT: Bio-oriented Technology Research Advancement Institution.

```

```

; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41297
; LENGTH: 1093
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41297

Query Match 44.7%; Score 38; DB 6; Length 1093;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATT 14
Db 98 HRESGSRPPQATS 111

RESULT 14
US-10-953-349-34917
; Sequence 34917, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34917
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34917

Query Match 44.1%; Score 37.5; DB 6; Length 132;
Best Local Similarity 53.3%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 HNDSPVTEQQATTW 15
Db 101 NNDSPLENT-QAAALW 114

RESULT 15
US-11-056-355B-7331
; Sequence 7331, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 7331
; LENGTH: 132
; TYPE: prt

```

```
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: {1}..(132)
; OTHER INFORMATION: Ceres Seq. ID no. 13498699
US-11-056-355B-7331
```

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Query Match      44.1%; Score 37.5; DB 7; Length 132;
Best Local Similarity 53.3%; Pred. No. 28;
Matches      8; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
```

```
QY      1 HNDSPVTEQQATTW 15
      :|||:| | | |
Db      101 NNDSPINT-QAALW 114
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Job time : 7.72727 secs
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**This Page Blank (uspto)**



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 54.5455 Seconds  
(without alignments)  
125.735 Million cell updates/sec

Title: US-10-758-165A-3

Perfect score: 74

Sequence: 1 RNNVLITDQQAATR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*
- 10: Geneseq2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	8 ADR10603	Adri0603 Horse Ige
2	74	100.0	424	5 AAM50103	Aam50103 Equine Ig
3	74	100.0	424	5 AAM50104	Aam50104 Equine Ig
4	74	100.0	566	9 AED15438	Aed15438 Equine Pr
5	74	100.0	566	10 AEE88000	Aee88000 Human pro
6	74	100.0	569	6 ABP96585	Abp96585 Horse Ige
7	49	66.2	15	7 ADC64568	Adc64568 Horse imm
8	43	58.1	417	9 AEB39722	Aeb39722 L. pneumo
9	43	58.1	452	9 AEB36305	Aeb36305 L. pneumo
10	43	58.1	580	5 ABG32001	Abg32001 Q. intest
11	43	58.1	580	8 ADP79623	Adp79623 Giardia i
12	41	55.4	312	3 AAY79995	Aay79995 Dog immu
13	41	55.4	312	8 ADR10601	Adri0601 Dog Ige e
14	41	55.4	312	8 ADN24060	Adn24060 Bacterial
15	41	55.4	417	2 AAW23067	Aaw23067 Canine Ig
16	41	55.4	426	2 AAR97753	Aar97753 Canine Ig
17	41	55.4	426	6 ABP96583	Abp96583 Dog Ige h
18	41	55.4	2000	6 ABR52669	Abr52669 Protein s
19	41	55.4	2000	7 ADK61774	Adk61774 Disease t
20	40	54.1	15	8 ADR10607	Adri0607 Pig Ige e
21	40	54.1	567	6 ABP96588	Abp96588 Pig Ige h
22	38	51.4	613	2 AAW73009	Aaw73009 Cobra ven
23	38	51.4	621	2 AAW73013	Aaw73013 Cobra ven

ALIGNMENTS

RESULT 1

ADRI0603  
ID ADR10603 standard; peptide; 15.AA.

XX AC ADR10603;

XX DT 21-OCT-2004 (first entry)

DE DE Horse Ige epitope recognised by monoclonal antibody 5.91, SEQ ID 3.

XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
horse.

XX OS Equus caballus.

XX FN WO2004065936-A2.

XX PD 05-AUG-2004.

XX PF 15-JAN-2004; 2004WO-US003566.

XX PR 16-JAN-2003; 2003US-0440472P.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

Novel antibody that specifically binds to mammalian Ige epitope, useful for testing an allergen reactivity of Ige sample, detecting mammalian Ige or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian Ige epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige. (I) is useful for testing an allergen reactivity of an Ige sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian Ige and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine Ige corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the

CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC horse IgE 5.91 recognition site.

XX  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15  
 |||||  
 Db 1 RNNVLIQTDDQATTR 15  
 |||||

RESULT 2  
 AAM50103  
 ID AAM50103 standard; protein; 424 AA.  
 XX  
 AC AAM50103;  
 XX  
 XX 02-SEP-2002 (first entry)  
 XX  
 XX Equine IgE heavy chain constant region C-epsilon allotype A.  
 DE  
 DE Cea; equine; horse; heavy chain; constant region; allotype a; IgE;  
 KW C-epsilon a; immunoglobulin E; antiallergic; allergy.  
 XX  
 XX Equus caballus.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..97  
 FT /note= "CH1 domain"  
 FT Domain 98..205  
 FT /note= "CH2 domain"  
 FT Domain 206..312  
 FT /note= "CH3 domain"  
 FT Domain 313..424  
 FT /note= "CH4 domain"  
 XX  
 XX WO200250280-A2.  
 XX  
 XX 27-JUN-2002.  
 XX  
 XX 20-DEC-2001; 2001WO-DE004810.  
 XX  
 XX 21-DEC-2000; 2000DE-01064415.  
 XX  
 XX (TIER-) TIERAERTLICHE HOCHSCHULE HANNOVER.  
 XX  
 XX Leibold W, Wagner B, Radbruch A;  
 XX  
 XX WPI; 2002-508803/54.  
 XX  
 XX N-PSDB; ABL61246.  
 XX  
 XX DNA sequence encoding part of an equine immunoglobulin G, useful for  
 XX preparing isotype-specific antibodies for diagnosis and treatment of  
 XX allergy in horses.  
 XX  
 XX Claim 1; Page 31-32; 37pp; German.  
 XX  
 XX This invention describes a novel DNA (I) encoding the constant region  
 XX (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The  
 XX products of the invention are capable of neutralising IgE activity and  
 XX have antiallergic activity. The polynucleotides of the invention are used  
 XX to produce recombinant IgE (II), and this is used to raise specific  
 XX monoclonal antibodies (MAB). Both (II) and MAB are useful for diagnosis,  
 XX particularly of allergy in horses, and MAB can also be used for treatment  
 XX of allergies. (I) make possible production of isotype-specific  
 XX antibodies, important for precise evaluation of the immune response. This

CC sequence represents a fragment of the equine IgG heavy chain constant  
 CC region C-epsilon allotype a (Cea), used in the method of the invention  
 CC for IgG-isotype recombinant immunoglobulin production

XX  
 XX  
 SQ Sequence 424 AA;

Query Match 100.0%; Score 74; DB 5; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15  
 |||||  
 Db 356 RNNVLIQTDDQATTR 370  
 |||||

RESULT 3  
 AAM50104  
 ID AAM50104 standard; protein; 424 AA.  
 XX  
 AC AAM50104;  
 XX  
 XX 02-SEP-2002 (first entry)  
 XX  
 XX Equine IgG heavy chain constant region C-epsilon allotype b.  
 DE  
 DE Ceb; equine; horse; heavy chain; constant region; allotype b; IgE;  
 KW C-epsilon b; immunoglobulin E; antiallergic; allergy.  
 XX  
 XX Equus caballus.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..97  
 FT /note= "CH1 domain"  
 FT Domain 98..205  
 FT /note= "CH2 domain"  
 FT Domain 206..312  
 FT /note= "CH3 domain"  
 FT Domain 313..424  
 FT /note= "CH4 domain"  
 XX  
 XX WO200250280-A2.  
 XX  
 XX 27-JUN-2002.  
 XX  
 XX 20-DEC-2001; 2001WO-DE004810.  
 XX  
 XX 21-DEC-2000; 2000DE-01064415.  
 XX  
 XX (TIER-) TIERAERTLICHE HOCHSCHULE HANNOVER.  
 XX  
 XX Leibold W, Wagner B, Radbruch A;  
 XX  
 XX WPI; 2002-508803/54.  
 XX  
 XX N-PSDB; ABL61247.  
 XX  
 XX DNA sequence encoding part of an equine immunoglobulin G, useful for  
 XX preparing isotype-specific antibodies for diagnosis and treatment of  
 XX allergy in horses.  
 XX  
 XX Claim 1; Page 34-36; 37pp; German.  
 XX  
 XX This invention describes a novel DNA (I) encoding the constant region  
 XX (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The  
 XX products of the invention are capable of neutralising IgE activity and  
 XX have antiallergic activity. The polynucleotides of the invention are used  
 XX to produce recombinant IgE (II), and this is used to raise specific  
 XX monoclonal antibodies (MAB). Both (II) and MAB are useful for diagnosis,  
 XX particularly of allergy in horses, and MAB can also be used for treatment  
 XX of allergies. (I) make possible production of isotype-specific  
 XX antibodies, important for precise evaluation of the immune response. This  
 XX sequence represents a fragment of the equine IgG heavy chain constant  
 XX region C-epsilon allotype b (Ceb), used in the method of the invention  
 XX for IgG-isotype recombinant immunoglobulin production

XX SQ Sequence 424 AA;  
Query Match 100.0%; Score 74; DB 5; Length 424;  
Best Local Similarity 100.0%; Pred. No. 8.6e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RNNVLIQTDOQATTR 15  
Db 356 RNNVLIQTDOQATTR 370

RESULT 4  
AED15438  
ID AED15438 standard; protein; 566 AA.  
XX AC AED15438;  
XX DT 01-DEC-2005 (first entry)  
XX DE Equine Protozoal Myeloencephalitis marker polypeptide, SEQ ID No:21.  
XX KW equine protozoal myeloencephalitis; genetic marker; diagnosis;  
XX KW sarcocystis neurona infection; protozoacide.  
XX OS Equidae.  
XX WO2005090593-A1.  
XX PD 29-SEP-2005.  
XX PF 21-MAR-2005; 2005WO-AU000401.  
XX PR 19-MAR-2004; 2004AU-00901448.  
XX PR 29-MAR-2004; 2004US-0556869P.  
XX PR 23-JUN-2004; 2004US-0581840P.  
XX (GENO-) GENOMICS RES PARTNERS PTY LTD.  
XX Brandon RB, Thomas MR;  
XX WPI; 2005-659146/67.  
XX N-PSDB; AED15437.  
XX New isolated Equine Protozoal Myeloencephalitis (EPM) marker  
XX polynucleotides and polypeptides, useful in diagnosing, monitoring and  
XX treating EPM in affected animals, e.g. horse.  
XX Claim 1; SEQ ID NO 21; 356pp; English.

XX The invention relates to isolated Equine Protozoal Myeloencephalitis  
XX (EPM) marker polynucleotide sequences selected from any of the fully  
XX defined sequences (SEQ ID NOS 1, 3, 5, 7, 8, 10, 12, 14, 16, 17, 18, 20,  
XX 22, 24, 26, 27, 28, 30, 32, 34-50, 52, 54, 55, 56, 57, or 422) in the  
XX specification. The EPM polynucleotide sequences encode EPM polypeptides  
XX (SEQ ID NOS 2, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 35, 53,  
XX or 58). Also described are: (1) a method of diagnosing the presence of  
XX EPM or Sarcocystis neurona infection in a test subject; (2) a method of  
XX treating, preventing, or inhibiting the development of EPM in a subject;  
XX (3) a nucleic acid construct comprising an EPM marker polynucleotide in  
XX operable connection with a regulatory element that is operable in a host  
XX cell; (4) an isolated host cell containing the nucleic acid construct;  
XX (5) a probe (SEQ ID NO. 59-421) comprising a nucleotide sequence that  
XX hybridizes under low stringency conditions to the polynucleotide; and (6)  
XX a solid or semi-solid support comprising at least one probe immobilized  
XX on it. The EPM marker polynucleotides, probes, EPM marker polypeptides,  
XX or antigen-binding molecules that are immuno-interactive with the EPM  
XX marker polypeptide, are useful for diagnosing the presence of EPM in a  
XX subject. The EPM marker polynucleotides and polypeptides are also useful  
XX for the diagnosis, monitoring, and treatment of EPM in affected animals.  
XX This sequence represents an EPM marker polypeptide.

XX SQ Sequence 566 AA;  
Query Match 100.0%; Score 74; DB 9; Length 566;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RNNVLIQTDOQATTR 15  
Db 499 RNNVLIQTDOQATTR 513

RESULT 5  
AEE88000  
ID AEE88000 standard; protein; 566 AA.  
XX AC AEE88000;  
XX DT 23-FEB-2006 (first entry)  
XX DE Human protein sequence #49.  
XX KW Diagnosis; immunity; stress; psychiatric disorder; tranquilizer.  
XX OS Homo sapiens.  
XX PN WO2005118810-A1.  
XX PD 15-DEC-2005.  
XX PF 03-JUN-2005; 2005WO-AU000794.  
XX PR 03-JUN-2004; 2004US-0576285P.  
XX PR 04-JUN-2004; 2004AU-00903003.  
XX (GENO-) GENOMICS RES PARTNERS PTY LTD.  
XX Brandon RB, Thomas MR;  
XX WPI; 2006-039470/04.  
XX N-PSDB; AEE87999.  
XX Determining presence or degree of a physiological response to stress or a  
XX related condition in a test subject, comprises detecting in the test  
XX subject aberrant expression of at least one stress marker gene.  
XX Claim 1; SEQ ID NO 136; 445pp; English.

XX The invention relates to a method of determining the presence or degree  
XX of a physiological response to stress or a related condition in a test  
XX subject comprising detecting in the test subject aberrant expression of  
XX at least one stress marker gene given in the specification. The invention  
XX also relates to a method of treating, preventing or inhibiting the  
XX development of stress in a subject, an isolated stress marker  
XX polynucleotide, a nucleic acid construct comprising a stress marker  
XX polynucleotide in operable connection with a regulatory element that is  
XX operable in a host cell, an isolated host cell containing the construct,  
XX a probe comprising a nucleotide sequence that hybridizes under at least  
XX low stringency conditions to the marker polynucleotide and a solid or  
XX semi-solid support comprising at least one probe immobilized on it. The  
XX stress marker polynucleotides, probes, stress marker polypeptides or  
XX antigen-binding molecules that are immuno-interactive with the stress  
XX marker polypeptide are useful for the manufacture of a kit for diagnosing  
XX the presence of a physiological response to stress in a subject. The  
XX methods are useful for determining the presence or degree of a  
XX physiological response to stress or a related condition in a test  
XX subject, and for treating, preventing or inhibiting the development of  
XX stress in a subject. The physiological response to stress is selected  
XX from physical stress, mood disorders, anxiety disorders, inflammation,  
XX pain, chronic fatigue syndrome, stress-induced headache, cancer, human  
XX immunodeficiency virus (HIV) infections, neurodegenerative diseases,  
XX gastrointestinal diseases, eating disorders, supranuclear palsy,  
XX ankyrotrophic lateral sclerosis, a decrease in immune function or  
XX immunosuppression, hemorrhagic stress, stress-induced psychotic episodes,  
XX eutthyroid sick syndrome, syndrome of inappropriate antidiuretic hormone

CC (ADH), overeating or obesity, infertility, head traumas, spinal cord  
 CC trauma, ischemic neuronal damage, excitotoxic neuronal damage, epilepsy,  
 CC cardiovascular diseases, stroke, immune dysfunctions, muscular spasms,  
 CC urinary incontinence, senile dementia, Alzheimer's disease, multi-infarct  
 CC dementia, amyotrophic lateral sclerosis, chemical dependencies and  
 CC addictions, drug and alcohol withdrawal symptoms, osteoporosis,  
 CC psychosocial dwarfism, hypoglycemia, hair loss, abnormal circadian rhythm  
 CC or disorders related to abnormal circadian rhythm. This sequence  
 CC represents a human protein used in the method of the invention.  
 XX  
 SQ Sequence 566 AA;

Query Match 100.0%; Score 74; DB 10; Length 566;  
 Best Local Similarity 100.0%; Pred. NO. 0.00012;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15  
 |||||  
 Db 499 RNNVLIQTDDQATTR 513

RESULT 6  
 ABP96585  
 ID ABP96585 standard; protein; 569 AA.

AC ABP96585;

XX  
 DT 28-MAY-2003 (first entry)

DE Horse IgE heavy chain amino acid sequence SEQ ID NO:30.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
 KW immune response; major histocompatibility complex; MHC; immunogenic;  
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.

XX Equus caballus.

XX WO2003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IgE, by identifying peptide eliciting CTL response to IgE  
 PT peptides naturally presented by major histocompatibility complex class I  
 PT protein.

PS Example 7; Page 157-160; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IgE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to

CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,  
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in  
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic  
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an IgE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention  
 XX  
 SQ Sequence 569 AA;

Query Match 100.0%; Score 74; DB 6; Length 569;  
 Best Local Similarity 100.0%; Pred. NO. 0.00012;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15  
 |||||  
 Db 501 RNNVLIQTDDQATTR 515

RESULT 7  
 ADC64568

ID ADC64568 standard; peptide; 15 AA.

XX ADC64568;

XX 18-DEC-2003 (first entry)

XX Horse immunoglobulin E, IgE, heavy chain immunogenic peptide P4.

DE Horse; immunoglobulin E; IgE; heavy chain; immunogen; allergy.

XX Equus caballus.

XX US2003087314-A1.

XX 08-MAY-2003.

XX 08-NOV-2001; 2001US-00052788.

XX 08-NOV-2001; 2001US-00052788.

XX (REGC ) UNIV CALIFORNIA.

XX Gershwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

XX Immunogenic composition comprising an isolated equine immunoglobulin E  
 PT polypeptide that induces production of antibodies which specifically bind  
 PT to equine immunoglobulin E.

XX Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that  
 CC specifically binds to equine IgE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an  
 CC antibody that specifically binds to equine IgE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-  
 CC (S6)), and collecting antiserum from the animal) and a kit for detection

CC of equine IgE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IgE. The  
 CC antibody is useful for detecting equine IgE protein in a biological  
 CC sample (serum) which involves contacting the sample with the antibody,  
 CC thus forming an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the  
 CC complex can be detected. The antibody is labelled using a second labelled  
 CC antibody. The peptides are useful for generating antibodies specific for  
 CC IgE which can serve as a diagnostic test for allergy. The present  
 CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic  
 CC peptide from the early portion of the C4 region.

XX SQ Sequence 15 AA;

Query Match 66.2%; Score 49; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.074;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IQTDDQATTR 15  
 Db 1 IQTDDQATTR 10  
 |||||

#### RESULT 8

ID AEB39722 standard; protein; 417 AA.

XX AC AEB39722;

DT 08-SEP-2005 (first entry)

XX L. pneumophila protein SEQ ID NO 4054.

DE detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

XX WO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004WO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP ) INST PASTEUR.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;  
 PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;  
 PI Jarraud S;

XX WPI; 2005-388305/40.

XX New genome of Legionella pneumophila Paris strain and derived

PT polypeptides, useful for detection or identification of the strain and

PT for treatment and prevention of infections.

XX Claim 3; SEQ ID NO 4054; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)  
 CC from Legionella pneumophila Paris strain. (I), and their related  
 CC sequences or fragments, are useful as primers and probes for detection  
 CC and amplification, including differentiation between the Paris and  
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant  
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
 CC specific antibodies (Ab), also used for detection/identification of  
 CC Legionella, and some (I), specifically those involved in synthesis of  
 CC surface proteins, are targets for identification of inhibitors. (II), or  
 CC vectors that contain (I), are useful as vaccines and immunogenic

CC compositions, for treatment and prevention of infections by L.  
 CC pneumophila. The present sequence represents the amino acid sequence of a  
 CC L. pneumophila protein.

XX SQ Sequence 417 AA;

Query Match 58.1%; Score 43; DB 9; Length 417;

Best Local Similarity 69.2%; Pred. No. 38;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIQTDQQAATT 14

Db 63 NNVLIPLEQQPPTT 75

||||| :|||

#### RESULT 9

AEB36305

ID AEB36305 standard; protein; 452 AA.

XX AC AEB36305;

DT 08-SEP-2005 (first entry)

XX L. pneumophila protein SEQ ID NO 637.

DE detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

XX WO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004WO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP ) INST PASTEUR.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;  
 PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;  
 PI Jarraud S;

XX WPI; 2005-388305/40.

XX New genome of Legionella pneumophila Paris strain and derived

PT polypeptides, useful for detection or identification of the strain and

PT for treatment and prevention of infections.

XX Claim 3; SEQ ID NO 637; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)  
 CC from Legionella pneumophila Paris strain. (I), and their related  
 CC sequences or fragments, are useful as primers and probes for detection  
 CC and amplification, including differentiation between the Paris and  
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant  
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
 CC specific antibodies (Ab), also used for detection/identification of  
 CC Legionella, and some (I), specifically those involved in synthesis of  
 CC surface proteins, are targets for identification of inhibitors. (II), or  
 CC vectors that contain (I), are useful as vaccines and immunogenic  
 CC compositions, for treatment and prevention of infections by L.  
 CC pneumophila. The present sequence represents the amino acid sequence of a  
 CC L. pneumophila protein.

XX SQ Sequence 452 AA;

Query Match 58.1%; Score 43; DB 9; Length 452;

Best Local Similarity 69.2%; Pred. No. 41;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLITDQOATT 14  
 Db 98 NNVLIPLEQOQPTT 110

RESULT 10  
 ABG32001  
 ID ABG32001 standard, protein; 580 AA.  
 XX AC ABG32001;  
 XX DT 06-AUG-2003 (revised)  
 XX DT 15-NOV-2002 (first entry)  
 XX DE Q. intestinalis arginine deiminase gene, QIAADIINT.  
 XX KW Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine;  
 XX KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;  
 XX KW auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.  
 XX OS Giardia intestinalis.  
 XX PN WO200244360-A2.  
 XX PD 06-JUN-2002.  
 XX PF 19-SEP-2001; 2001WO-US029184.  
 XX PR 28-NOV-2000; 2000US-00723546.  
 XX PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
 XX PI Clark MA;  
 XX PS WPI; 2002-619003/66.  
 XX DR Compound for treating tumor such as melanoma, hepatoma or sarcoma in a  
 XX PT patient, comprises arginine deiminase covalently bonded by a linking  
 XX PT group such as succinimide to polyethylene glycol.  
 XX PS Disclosure; Fig 12; 59pp; English.  
 XX CC The invention discloses a compound comprising arginine deiminase (ADI)  
 XX CC covalently bonded by a linking group to polyethylene glycol (PEG) having  
 XX CC a total weight average molecular weight of about 1000-50000. Also  
 XX CC disclosed is a method for enhancing the circulating half life or the  
 XX CC tumoricidal activity of arginine deiminase by modifying the arginine  
 XX CC deiminase by covalently bonding the arginine deiminase by a linking group  
 XX CC to PEG. Normal cells can synthesise arginine from citrulline in a 2 step  
 XX CC process catalysed by argininosuccinate synthase and argininosuccinate  
 XX CC lyase. In contrast, many cancerous cells do not express argininosuccinate  
 XX CC synthase and are, therefore, auxotrophic for arginine. Arginine deiminase  
 XX CC eliminates the conversion of arginine to citrulline and can be used to  
 XX CC eliminate arginine from the cancerous cells. The compound is useful for  
 XX CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or  
 XX CC for treating and inhibiting metastases in a patient. When compared to  
 XX CC native arginine deiminase the compound retains most of its enzymatic  
 XX CC activity, is far less antigenic, has a greatly extended circulating half-  
 XX CC life, and is much more efficacious in the treatment of tumours. The  
 XX CC sequence presented is the Giardia intestinalis arginine deiminase gene,  
 XX CC QIAADIINT. (Updated on 06-AUG-2003 to correct OS field.)  
 XX SQ Sequence 580 AA;

Query Match 58.1%; Score 43; DB 5; Length 580;  
 Best Local Similarity 57.1%; Pred. No. 55;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLITDQOATT 15  
 Db 168 NNWVFRDQOITTR 181

RESULT 11  
 ADP79623  
 ID ADP79623 standard; protein; 580 AA.  
 XX AC ADP79623;  
 XX DT 04-NOV-2004 (first entry)  
 XX DE Giardia intestinalis arginine deiminase.  
 XX KW Arginine deiminase; cytosolic; virucide; viral replication;  
 XX KW nitric oxide synthesis; tumour; liver function; enzyme.  
 XX OS Giardia intestinalis.  
 XX PN WO2004046309-A2.  
 XX PD 03-JUN-2004.  
 XX PF 29-SEP-2003; 2003WO-US030770.  
 XX PR 18-NOV-2002; 2002US-0427497P.  
 XX PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
 XX PI Clark MA;  
 XX PS WPI; 2004-431965/40.  
 XX DR Inhibiting replication of viruses in individual, involves administering  
 XX PT composition comprising arginine deiminase bonded to polyethylene glycol,  
 XX PT to individual.  
 XX PS Claim 18; SEQ ID NO 17; 89pp; English.  
 XX CC The invention relates to inhibiting the replication of one or more  
 XX CC viruses in an individual and involves administering to the individual a  
 XX CC composition comprising an arginine deiminase bonded to polyethylene  
 XX CC glycol. The method is useful for inhibiting replication of one or more  
 XX CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
 XX CC where the arginine deiminase is derived from Mycoplasma e.g. M. arginini,  
 XX CC M. hominis, M. arthritidis and its combination. It is useful for treating  
 XX CC an individual who is suspected of having been exposed to one or more  
 XX CC viruses, for modulating nitric oxide levels in an individual, or for  
 XX CC selectively inhibiting viral replication in an individual. The method is  
 XX CC also useful for treating a tumour and inhibiting replication of one ore  
 XX CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
 XX CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
 XX CC useful for improving liver function in an individual. The present  
 XX CC sequence represents a Giardia intestinalis arginine deiminase.  
 XX SQ Sequence 580 AA;

Query Match 58.1%; Score 43; DB 8; Length 580;  
 Best Local Similarity 57.1%; Pred. No. 55;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLITDQOATT 15  
 Db 168 NNWVFRDQOITTR 181

RESULT 12  
 ADRI0601  
 ID ADRI0601 standard; peptide; 15 AA.  
 XX AC ADRI0601;  
 XX DT 21-OCT-2004 (first entry)  
 XX DE Dog IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.  
 XX XX

KW Antiasthmatic; Anti-allergic; Immunosuppressive; IgE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO2004065936-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 XX 15-JAN-2004; 2004WO-US003566.  
 PF  
 XX  
 XX 16-JAN-2003; 2003US-0440472P.  
 PR  
 XX  
 XX (UUNC-) UNIV NORTH CAROLINA STATE.  
 PA  
 XX Hammerberg B;  
 XX  
 XX WPI; 2004-593545/57.  
 DR  
 XX  
 XX Novel antibody that specifically binds to mammalian IgE epitope, useful  
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 PT or treating asthma or anaphylactic shock.  
 XX  
 XX  
 XX Example 6; Page 9; 14pp; English.  
 PS  
 XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IgE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 55.4%; Score 41; DB 8; Length 15;  
 Best Local Similarity 64.3%; Pred. No. 2.1;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RNNVLIQTDDQATT 14  
 ||: ||||| ||  
 DB 1 RNDSPITQDQYTTT 14  
 RESULT 13  
 AAY79995  
 ID AAY79995 standard; protein; 312 AA.  
 XX  
 AC AAY79995;  
 XX  
 DT 15-MAY-2000 (first entry)  
 XX  
 XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.  
 DE  
 XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.  
 XX  
 OS Canis sp.  
 XX  
 XX WO9967293-A1.  
 PN  
 XX 29-DEC-1999.  
 PD  
 XX

PF 21-JUN-1999; 99WO-US013959.  
 XX  
 PR 20-JUN-1998; 98US-00100287.  
 XX  
 PA (UNBI-) UNITED BIOMEDICAL INC.  
 XX  
 PI Wang CY, Walfield AM;  
 XX  
 DR WPI; 2000-160578/14.  
 XX  
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.  
 PT  
 XX  
 XX Example 1; Page 66-68; 155pp; English.  
 PS  
 XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention  
 XX  
 XX Sequence 312 AA;  
 SQ  
 Query Match 55.4%; Score 41; DB 3; Length 312;  
 Best Local Similarity 64.3%; Pred. No. 63;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RNNVLIQTDDQATT 14  
 ||: ||||| ||  
 DB 255 RNDSPITQDQYTTT 268  
 RESULT 14  
 ADN24060  
 ID ADN24060 standard; protein; 312 AA.  
 XX  
 AC ADN24060;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 XX Bacterial polypeptide #6713.  
 DE  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 XX US2003233675-A1.  
 PN  
 XX 18-DEC-2003.  
 PD  
 XX 20-FEB-2003; 2003US-00369493.  
 XX  
 XX 21-FEB-2002; 2002US-0360039P.  
 PR  
 XX (CAOY/) CAO Y.  
 PA

PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX  
 DR WPI; 2004-061375/06.  
 XX  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 FT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 PT  
 XX  
 XX Claim 1; SEQ ID NO 6713; 122pp; English.  
 PS  
 XX  
 CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 312 AA;  
 Query Match 55.4%; Score 41; DB 8; Length 312;  
 Best Local Similarity 57.1%; Pred. No. 63;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 NNVLITDQQAATR 15  
 Db 159 DNVLIQKDENTAR 172  
 :|||||:|:|  
 :|||:|:|  
 RESULT 15  
 AAW23067  
 ID AAW23067 standard; protein; 417 AA.  
 XX  
 AC AAW23067;  
 XX  
 XX 30-JUN-2005 (revised)  
 DT 16-JUN-2005 (revised)  
 DT 19-FEB-1998 (first entry)  
 XX  
 XX Canine IgE heavy chain constant region (exon 1-4 product).  
 DE  
 XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 XX hypersensitivity; therapy; dog; antisense; immunomodulation.  
 KW  
 XX Canis familiaris.  
 OS  
 XX Key Location/Qualifiers  
 FH  
 FT Misc-difference 55 /note= "encoded by ACC"  
 FT Misc-difference 56 /note= "encoded by TAC"  
 FT

FT Misc-difference 67 /note= "encoded by GCC"  
 FT Misc-difference 83 /note= "encoded by NNT"  
 FT Misc-difference 174 /note= "encoded by GGN"  
 FT Misc-difference 175 /note= "encoded by NNG"  
 FT Misc-difference 176 /note= "encoded by TGN"  
 FT Misc-difference 203 /note= "encoded by TCC"  
 FT Misc-difference 204 /note= "encoded by GAC"  
 FT  
 XX W09730156-A2.  
 FN  
 XX 21-AUG-1997.  
 PD  
 XX 14-FEB-1997; 97WO-US002322.  
 PF  
 XX 14-FEB-1996; 96US-00601197.  
 PR  
 XX (IDEX-) IDEXX LAB INC.  
 PA  
 XX Mermer B, Harris RA, Siefring AE;  
 PI  
 XX WPI; 1997-425031/39.  
 DR  
 XX N-PSDB; AAT79278.  
 DR  
 XX Isolated canine IgE heavy chain constant region DNA - useful to develop  
 PT products for treatment of canine allergies and for immunomodulation in  
 PT dogs.  
 FT  
 XX Disclosure; Page 35-39; 59pp; English.  
 PS  
 XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE  
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat Type I immediate hypersensitivity, and for immunomodulation  
 CC  
 CC Revised record issued on 30-JUN-2005 : Typo in comments  
 CC  
 XX Sequence 417 AA;  
 Query Match 55.4%; Score 41; DB 2; Length 417;  
 Best Local Similarity 64.3%; Pred. No. 88;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 OY 1 RNNVLIQTDDQQAAT 14  
 Db 352 RNDSPITQTDQVTTT 365  
 :||:|||||  
 :||:|||||  
 Search completed: August 30, 2006, 04:22:06  
 Job time : 55:5455 secs



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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 8.93939 Seconds  
(without alignments)  
161.448 Million cell updates/sec

Title: US-10-758-165a-3  
Perfect score: 74  
Sequence: 1 RNNVLITDQQATT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	60.8	917	2 F95884	probable sensory h
2	43.5	58.8	285	2 H84219	hypothetical prote
3	43	58.1	580	2 T45064	arginine deiminase
4	41	55.4	312	2 T32446	hypothetical prote
5	41	55.4	312	2 A89460	protein H42K12.1 l
6	41	55.4	2145	2 S61041	glutamate synthase
7	39	52.7	263	2 E85042	hypothetical prote
8	39	52.7	716	2 H84421	probable receptor-
9	38	51.4	138	2 G97191	probable membrane
10	38	51.4	829	2 A12531	hypothetical prote
11	38	51.4	1827	1 A23945	sucrose alpha-gluc
12	37	50.0	128	1 H64842	probable translati
13	37	50.0	128	2 F90785	hypothetical prote
14	37	50.0	128	2 F85645	hypothetical prote
15	36.5	49.3	1017	2 S67804	LRG1 protein - yea
16	36	48.6	140	2 S72252	hemoglobin, extrac
17	36	48.6	205	2 B88095	protein F39E9.5 [1
18	36	48.6	407	2 A22150	serine proteinase
19	36	48.6	412	2 T24441	hypothetical prote
20	36	48.6	433	2 C70163	GTP-binding protei
21	36	48.6	441	2 G98136	histidine protein
22	36	48.6	441	2 B95261	probable sensor hi
23	36	48.6	468	2 A53889	protein-cytosine-p
24	36	48.6	468	2 T43622	targeted effector
25	36	48.6	468	2 S01054	virulence protein
26	36	48.6	487	1 S07062	glutamate receptor
27	36	48.6	487	2 T51201	kinase-binding pr
28	36	48.6	962	2 C81060	translation initia
29	36	48.6	967	2 C70831	probable mmpL4 pro

30	36	48.6	1157	2 AD1728	ATP-dependent deox
31	36	48.6	1418	2 T15232	hypothetical prote
32	36	48.6	1449	2 T20181	hypothetical prote
33	36	48.6	1464	2 JCS144	murinoglobulin pre
34	36	48.6	1584	2 T20180	hypothetical prote
35	36	48.6	1586	2 T20179	hypothetical prote
36	36	48.6	2021	2 AD2267	serins/threonine k
37	35	47.3	185	2 T14523	hypothetical prote
38	35	47.3	225	2 AC0587	KDP operon transcr
39	35	47.3	225	2 B90719	transcription regu
40	35	47.3	225	2 C85569	hypothetical prote
41	35	47.3	225	2 E64804	transcription regu
42	35	47.3	252	2 T20321	hypothetical prote
43	35	47.3	276	2 B84597	probable disease r
44	35	47.3	345	2 S73498	MG456 homolog K05
45	35	47.3	386	2 T09019	phosphoprotein pho

ALIGNMENTS

RESULT 1  
F95884

probable sensory histidine kinase protein [imported] - Sinorhizobium meliloti (strain 10  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: F95884  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: F95884  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-917 <KUR>  
A:Cross-references: UNIPROT:Q92WJ7; UNIPARC:UPI00000CB4C5; GB:AL591985; PIDN:CAC48742.1;  
A:Experimental source: strain 1021, megaplasmid pSymB  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Smb20356  
A:Genome: plasmid

Query Match 60.8%; Score 45; DB 2; Length 917;  
Best Local Similarity 57.1%; Pred. No. 3.6;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNNVLITDQQATT 14  
|||:::|||  
Db 188 RNEVVVQTEKTATT 201

RESULT 2  
H84219

hypothetical protein Vng0617h [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: H84219  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: H84219

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-285 <STO>  
A;Cross-references: UNIPROT:Q9HRN4; UNIPARC:UPI00000636A7; GB:AE004437; NID:gi10580210; F  
C;Genetics:  
A;Gene: VNG0617H

Query Match 58.8%; Score 43.5; DB 2; Length 285;  
Best Local Similarity 58.8%; Pred. No. 1.8;  
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 2 NNVLQTDQ--ATTR 15  
|||||:|:|:|  
Db 212 NNVLQTDSEVELTTR 228  
|||||:|:|:|

RESULT 3  
T45064  
arginine deiminase (EC 3.5.3.6) [validated] - Giardia intestinalis  
C;Species: Giardia intestinalis  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T45064  
R;Knudler, L.A.; Skyeve, E.O.; Stewart, T.S.; Schofield, P.J.; Edwards, M.R.  
J. Biol. Chem. 273, 4470-4477, 1998  
A;Title: Cloning and expression of a prokaryotic enzyme, arginine deiminase, from a prim  
A;Reference number: 222902; MUID:98136144; PMID:9468500  
A;Accession: T45064  
A;Status: preliminary;  
A;Molecule type: DNA  
A;Residues: 1-580 <KNO>  
A;Cross-references: UNIPROT:Q27657; UNIPARC:UPI000004CCBB; EMBL:U49236; PIDN:AAC06116.1  
A;Experimental source: strain Fortland 1  
C;Function:  
A;Description: EC 3.5.3.6 [validated, MUID:98136144]  
C;Superfamily: Giardia intestinalis arginine deiminase  
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 580;  
Best Local Similarity 57.1%; Pred. No. 5.2;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATR 15  
||:|:|:|:|:|  
Db 168 NNWFMRDQAATR 181  
||:|:|:|:|:|

RESULT 4  
T32446  
hypothetical protein H42K12.1 - Caenorhabditis elegans (fragment)  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 05-Oct-2004  
C;Accession: T32446  
R;Maggi, L.; Harper, M.  
submitted to the EMBL Data Library, September 1997  
A;Description: The sequence of C. elegans cosmid H42K12.  
A;Reference number: Z21169  
A;Accession: T32446  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-312 <MAG>  
A;Cross-references: UNIPARC:UPI000017A469; EMBL:AF026207; PIDN:AAB71265.1; GSPDB:GN00028  
A;Experimental source: strain Bristol N2; clone H42K12  
C;Genetics:  
A;Gene: CESP:H42K12.1  
A;Map position: X  
A;Introns: 4/2; 40/3; 106/1; 167/1; 196/2; 251/3

Query Match 55.4%; Score 41; DB 2; Length 312;  
Best Local Similarity 57.1%; Pred. No. 6.1;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATR 15  
:|||||:|:|:|

Db 159 DNVLQKDEENTAR 172

RESULT 5

A89460

protein H42K12.1 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 31-Dec-2004

C;Accession: A89460

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: A89460

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-312 &lt;STO&gt;

A;Cross-references: UNIPARC:UPI000017A469; GB:chr\_X; PIDN:AAB71265.1; PID:92435556; GSPDB

A;Note: Similar to protein kinase

C;Genetics:

A;Gene: H42K12.1

A;Map position: X

Query Match

Best Local Similarity

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATR 15

:|||||:|:|:|

Db 159 DNVLQKDEENTAR 172

RESULT 6

S61041

glutamate synthase (NADH2) (EC 1.4.1.14) gltI precursor [similarity] - yeast (Saccharomy

N;Alternate names: protein D1448; protein YDL171c

C;Species: Saccharomyces cerevisiae

C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 12-Jul-2004

C;Accession: S61041; S67723

R;Pohl, T.M.

submitted to the EMBL Data Library, November 1995

A;Reference number: S61010

A;Accession: S61041

A;Molecule type: DNA

A;Residues: 1-2145 &lt;POH&gt;

A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z67750; NID:gi1061256; PIDN:CAA91574.1; P

R;Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67708

A;Accession: S67723

A;Molecule type: DNA

A;Residues: 1-2145 &lt;POW&gt;

A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z74219; NID:gi1431273; PIDN:CAA98745.1; P

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGB:GLT1

A;Cross-references: SGD:S0002330; MIPS:YDL171c

A;Map position: 4L

C;Superfamily: glutamate synthase (NADH/NADPH), eukaryotic type

C;Keywords: 3Fe-4S; metalloprotein; oxidoreductase; transmembrane protein

F;1-53/Domain: propeptide #status predicted &lt;PRO&gt;

F;54-2145/Product: glutamate synthase #status predicted &lt;MAT&gt;

F;1077-1093/Domain: transmembrane #status predicted &lt;TM1&gt;

F;1172-1188/Domain: transmembrane #status predicted &lt;TM2&gt;

F;54/Active site: Cys #status predicted

F;1185,1191,1196/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match

Best Local Similarity

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATR 15

:|||||:|:|:|

Qy 1 RNNVLIQTDOQATT 14  
| : : : : : |  
Db 1145 RNNVVQTGQLRT 1158

## RESULT 7

E85042  
hypothetical protein AT4g03350 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: E85042  
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; MUID:20083488; PMID:10617198  
A;Accession: E85042  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-263 <STO>  
A;Cross-references: UNIPROT:Q9ZQZ6; UNIPARC:UPI000000A63C9; GB:NC\_001268; NID:g7270205; E  
C;Genetics:  
A;Gene: AT4g03350  
A;Map position: 4

Query Match 52.7%; Score 39; DB 2; Length 263;  
Best Local Similarity 50.0%; Pred. No. 12;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATT 14  
| : : : : : |  
Db 145 RTNQVQTTEQAST 158

## RESULT 8

H84421  
probable receptor-like protein kinase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004  
C;Accession: H84421  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: H84421  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-716 <STO>  
A;Cross-references: UNIPROT:Q9ZU46; UNIPARC:UPI000000A1C90; GB:AE002093; NID:g4262228; PT  
C;Genetics:  
A;Gene: At2g01210  
A;Map position: 2  
C;Superfamily: Receptor-like protein kinase

Query Match 52.7%; Score 39; DB 2; Length 716;  
Best Local Similarity 53.3%; Pred. No. 38;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATT 15  
: : : : : |  
Db 568 QSNRIIQTDOQPQR 582

## RESULT 9

G97191  
probable membrane protein [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: G97191  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4836, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G97191  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-138 <KUR>  
A;Cross-references: UNIPROT:Q97GK0; UNIPARC:UPI000000CA4D0; GB:AE001437; PIDN:AAK80322.1;  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC2366

Query Match 51.4%; Score 38; DB 2; Length 138;  
Best Local Similarity 53.8%; Pred. No. 9;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQOQATT 14  
| : : : : : |  
Db 42 NNILAQSGQAST 54

## RESULT 10

AI2531  
hypothetical protein alr7540 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AI2531  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AI2531  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-829 <KUR>  
A;Cross-references: UNIPROT:Q8ZSH0; UNIPARC:UPI000000CCD69; GB:AP003602; PIDN:BA877183.1;  
C;Genetics:  
A;Experimental source: strain PCC 7120

Query Match 51.4%; Score 38; DB 2; Length 829;  
Best Local Similarity 70.0%; Pred. No. 69;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NNVLITDQOQ 11  
| : : : : : |  
Db 591 NNVLIQADRE 600

## RESULT 11

A23945  
sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) - rabbit  
N;Alternate names: small intestinal sucrase/isomaltase (SI)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 24-May-1996  
C;Accession: A23945; B25987; A29163  
R;Hunziker, W.; Spiess, M.; Semenza, G.; Lodish, H.F.  
Cell 46, 227-234, 1986  
A;Title: The sucrase-isomaltase complex: primary structure, membrane-orientation, and ev  
A;Reference number: A23945; MUID:86245068; PMID:3755079  
A;Accession: A23945  
A;Molecule type: mRNA  
A;Residues: 1-1827 <HUN>  
A;Cross-references: UNIPARC:UPI00001729E8  
R;Stoetrom, H.; Noren, O.; Christensen, L.A.; Wacker, H.; Spiess, M.; Bigler-Meier, B.  
FEBS Lett. 148, 321-325, 1982  
A;Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-iso  
A;Reference number: A25987; MUID:83105704; PMID:7152027  
A;Accession: B25987  
A;Molecule type: protein  
A;Residues: 2-32, 'XXX', 36-38; 1008, 'N', 1010-1014, 'E' <SU2>

A;Cross-references: UNIPARC:UPI00001729E9; UNIPARC:UPI00001729EA  
R;Frank, G.; Brunner, J.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H.  
FEBS Lett. 96, 183-188, 1978  
A;Title: The hydrophobic anchor of small-intestinal sucrase-isomaltase. N-terminal sequence  
A;Reference number: A29163; MUID:79086207; PMID:729784  
A;Accession: A29163  
A;Molecule type: protein  
A;Residues: 2, 'VNA', 6-32, 'XXX', 36-38 <FRA>  
A;Cross-references: UNIPARC:UPI00001729EB  
A;Comment: Carbohydrate analysis of the mature enzyme complex indicates both N- and O-linked  
C;Complex: the two product chains remain associated after cleavage  
C;Function: <ISM>  
A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic  
A;Pathway: carbohydrate digestion  
C;Function: <SUC>  
A;Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glucose  
A;Pathway: carbohydrate digestion  
C;Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology  
C;Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m  
F;2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <ISO>  
F;13-32/Domain: membrane associated #status predicted <TMW>  
F;43-65/Region: serine/threonine-rich  
F;63-109/Domain: trefoil homology <TRF1>  
F;189-840/Domain: sucrase/isomaltase homology <SIM>  
F;931-977/Domain: trefoil homology <TRF2>  
F;1008-1827/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental <SUC>  
F;1062-1734/Domain: sucrase/isomaltase homology <SIM2>  
F;12/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F;99,455,859,896,904,1235,1303,1325,1340,1354,1368,1403,1535,1575,1748,1763,1799/Binding  
F;1007-1008/Cleavage site: Arg-Ile (trypsin) #status predicted  
Query Match 51.4%; Score 38; DB 1; Length 1827;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 NNVLITDQQAQTR 15  
Db 144 NNVLTTESQANR 157

RESULT 12  
H64842  
Probable translation initiation regulator b1010 - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2004  
C;Accession: H64842  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: H64842  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-128 <BLAT>  
A;Cross-references: UNIPROT:P75896; UNIPARC:UPI000013ASE1; GB:AE000202; GB:U000096; NID:9  
A;Experimental source: strain K-12, substrain MG1655  
C;Superfamily: translation initiation inhibitor, TdcF type  
Query Match 50.0%; Score 37; DB 1; Length 128;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 NNVLITDQQAQTR 15  
Db 40 NNVLFAADDPKAQTR 53

RESULT 13  
H90785  
Hypothetical protein ECs1256 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 31-Dec-2004

C;Accession: H90785  
R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H90785  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-128 <HAY>  
A;Cross-references: UNIPROT:Q8XAU5; UNIPARC:UPI00000D067E; GB:BA000007; PIDN:BA034679.1;  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECs1256  
C;Superfamily: translation initiation inhibitor, TdcF type  
Query Match 50.0%; Score 37; DB 2; Length 128;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 NNVLITDQQAQTR 15  
Db 40 NNVLFAADDPKAQTR 53

RESULT 14  
H85645  
Hypothetical protein Z1509 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Dec-2004  
C;Accession: F85645  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: F85645  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-128 <STO>  
A;Cross-references: UNIPROT:Q8XAU5; UNIPARC:UPI00000D067E; GB:AE005174; NID:gl2514367; P  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z1509  
C;Superfamily: translation initiation inhibitor, TdcF type  
Query Match 50.0%; Score 37; DB 2; Length 128;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 NNVLITDQQAQTR 15  
Db 40 NNVLFAADDPKAQTR 53

RESULT 15  
S67804  
LRG1 protein - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein D0764; protein YDL240w  
C;Species: Saccharomyces cerevisiae  
C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: S67804; S43158; S47956  
R;Alt-Moerbe, J.; Schneider, C.; Moro, M.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67798  
A;Accession: S67804  
A;Molecule type: DNA  
A;Residues: 1-1017 <ALT>  
A;Cross-references: UNIPROT:P35688; UNIPARC:UPI000012E93A; EMBL:Z74288; NID:gl431407; PI  
R;Muehler, A.; Xu, G.; Wells, R.; Hollenberg, C.P.; Pipersberg, W.  
submitted to the EMBL Data Library, March 1994  
A;Description: LRG1 is expressed during sporulation in Saccharomyces cerevisiae and cont

A;Reference number: S43158  
A;Accession: S43158  
A;Molecule type: DNA  
A;Residues: 1-530,'Q','S',767-790,'T',792-820,'Q',822-837,'S',839-848,'L',850-859  
A;Cross-references: UNIPARC:UPI0000168CBB; EMBL:X79453; NID:G468734; PID:G468735  
R;Mueller, L.; Xu, G.; Wells, R.; Hollenberg, C.P.; Piepersberg, W.  
Nucleic Acids Res. 22, 3151-3154, 1994  
A;Title: LRG1 is expressed during sporulation in *Saccharomyces cerevisiae* and contains a  
A;Reference number: S47956; MUID:94344779; PMID:8065929  
A;Accession: S47956  
A;Molecule type: DNA  
A;Residues: 28-89;98-136,'MF',139-148;157-184;419-474;755-765,'S',767-790,'T',792-820,'Q'  
A;Cross-references: UNIPARC:UPI000017B2C8; UNIPARC:UPI000017B2C9; UNIPARC:UPI000017B2CA;  
C;Genetics:  
A;Gene: SGD:LRG1  
A;Cross-references: SGD:S0002399; MIPS:YDL240w  
A;Map position: 4L  
C;Keywords: transmembrane protein  
F;28-89/Domain: LIM metal-binding repeat homology <LIM1>  
F;98-148/Domain: LIM metal-binding repeat homology <LIM2>  
F;157-184/Domain: LIM metal-binding repeat homology <LIM3>  
F;348-364/Domain: transmembrane #status predicted <TM1>  
F;419-474/Domain: LIM metal-binding repeat homology <LIM4>  
F;487-503/Domain: transmembrane #status predicted <TM2>

Query Match 49.3%; Score 36.5; DB 2; Length 1017;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

QY 3 NVLIQTD-----QQATTR 15  
|::||| |::||  
Db 583 NLVIQTDPPSSSQVSTR 600

Search completed: August 30, 2006, 04:30:57  
Job time : 9.93939 secs

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Result No.	Score	Query			DB	ID	Description
		Match	Length	Count			
1	47	63.5	2081	2	Q9LH98	arabidopsis	
2	45	60.8	917	2	Q92WJ7	rhizobium m	
3	44	59.5	649	2	Q54AY3	dictyosteli	
4	44	59.5	649	2	Q55B16	dictyosteli	
5	43.5	58.8	285	2	Q9HRN4	halobacteri	
6	43	58.1	161	2	Q5C614	schistosoma	
7	43	58.1	416	2	Q5WV87	legionella	
8	43	58.1	417	2	Q5X3U5	legionella	
9	43	58.1	463	2	Q5ZU51	legionella	
10	43	58.1	505	2	Q7R036	giardia lam	
11	43	58.1	580	2	Q27657	giardia lam	
12	41.5	56.1	854	2	Q7ZX14	xenopus lae	
13	41	55.4	106	2	Q8H475	oryza sativ	
14	41	55.4	247	2	Q6FP28	candida gla	
15	41	55.4	260	2	Q4SVP5	tetradodon n	
16	41	55.4	540	2	Q4RX65	tetradodon n	
17	41	55.4	550	2	Q7XUQ6	oryza sativ	
18	41	55.4	835	2	Q3M1K9	anabaena va	
19	41	55.4	2141	2	Q6CMK0	kluveromyc	
20	41	55.4	2144	1	GLT1	YEAST	
21	41	55.4	2152	2	Q6PLS3	candida gla	
22	41	55.4	2195	2	Q75917	ashbya goss	
23	41	55.4	4936	2	Q6D5C2	erwinia car	
24	40	54.1	95	2	Q37FN1	rhodopsedu	
25	40	54.1	135	2	Q5QVD0	idiomarina	
26	40	54.1	136	2	Q9XR04	ambystoma m	
27	40	54.1	136	2	Q9XR05	ambystoma m	
28	40	54.1	357	2	Q3GQX7	psychrobact	
29	40	54.1	828	2	Q6WA42	parachlamyd	
30	39	52.7	166	2	Q74K19	lactobacilli	
31	39	52.7	263	2	Q9ZQZ6	arabidopsis	

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GN OrderedLocusNames=RB0342; ORFNames=SMB20356;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymb.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie J.,
RA Golding B., Puhler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
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CC -----
CC EMBL; ALS91985; CAC48742.1; -; Genomic_DNA.
DR PIR; P95884; P95884.
DR HSSP; P52934; 1QMP.
DR BioCyc; SMEL382:SMB20356-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .); IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR003660; His_kin_HAMP.
DR InterPro; IPR004358; His_kin_like_C.
DR InterPro; IPR003661; His_kin_N.
DR InterPro; IPR005467; His_kinase.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF02518; HisKA; 1.
DR Pfam; PF00072; Response_reg; 3.
DR PRINTS; PR00344; BCRLSENSOR.
DR ProDom; PD000039; Response_reg; 2.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HisKA; 1.
DR SMART; SM00448; REC; 2.
DR PROSITE; PS50885; HAMP; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 2.
KW Complete proteome; Kinase; Plasmid.
SQ SEQUENCE 917 AA; 100822 MW; 23847F2374CE99A1 CRC64;

Query Match 60.8%; Score 45; DB 2; Length 917;
Best Local Similarity 57.1%; Pred. No. 31;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
Db 188 RNEVVVQIEKATT 201

RESULT 3
Q54AY3_DICDI PRELIMINARY; PRT; 649 AA.
AC Q54AY3
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DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=DDB0215056;

Query Match 60.8%; Score 45; DB 2; Length 917;
Best Local Similarity 57.1%; Pred. No. 31;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
Db 188 RNEVVVQIEKATT 201

RESULT 3
Q54AY3_DICDI PRELIMINARY; PRT; 649 AA.
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DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=DDB0215056;
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OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Feider M., Thangavelu M., Johnson D.,
RA Knights A., Loulseghe H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 435:43-57 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AAP101000301; EAL60430.1; -; Genomic_DNA.
DR KW Hypothetical protein.
SQ SEQUENCE 649 AA; 77580 MW; B366A94429ECDD53 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 649;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIQTDDQATT 14
Db 611 NNIIITQQQKPT 623

RESULT 4
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AC Q55B16;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=DDB0218848;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
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RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loulseghe H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzner M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuapa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBS whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAF10100013; EAL171869.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 649 AA; 77580 MW; B366AD152ACDDA23 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 649;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQDQATT 14
Db 611 NNVLITDQDQKPT 623

RESULT 5
Q9HRN4 HALSA
ID O9HRN4 HALSA PRELIMINARY; PRT; 285 AA.-
AC O9HRN4
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Vng0617h.
GN OrderedLocusNames=VNG0617H;
OS Halobacterium salinarum (Halobacterium halobium).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Laaky S.R., Baliga N.S., Thorsson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlshocher M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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CC -----
DR EMBL; AE005010; AAG19124.1; -; Genomic_DNA.
DR PIR; H84219; H84219.
DR BIOCyc; HSP64091:VNG0617H-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 285 AA; 29163 MW; 31223D1A949BC1B3 CRC64;

Query Match 58.8%; Score 43.5; DB 2; Length 285;
Best Local Similarity 58.8%; Pred. No. 15;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

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Qy 2 NNVLITDQDQ---ATTR 15
Db 212 NNVLITDQDSELTTR 228

RESULT 6
Q5C614 SCHJA
ID Q5C614 SCHJA PRELIMINARY; PRT; 161 AA.
AC Q5C614;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 2.
DT 07-FEB-2006, entry version 5.
DE SUCHG07893 protein (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
RA Han Z.-G.;
RT "New Perspectives on Host-parasite Interplay by Comparative
RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
RT Schistosoma japonicum.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY808851; AAX24740.2; -; mRNA.
SQ SEQUENCE 161 AA; 18352 MW; 1A6BF6544526AE04 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 161;
Best Local Similarity 57.1%; Pred. No. 9;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQDQATT 15
Db 84 NNVLITDQDQKPSR 97

RESULT 7
Q5WV87 LEGPL
ID Q5WV87 LEGPL PRELIMINARY; PRT; 416 AA.
AC Q5WV87;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
GN OrderedLocusNames=lp11930;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazale C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
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CC -----
DR EMBL; CR628337; CAH16170.1; -; Genomic_DNA.
DR Legioblast; lp11930; -.
KW Complete proteome; Hypothetical protein.

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SQ SEQUENCE 416 AA; 48862 MW; OE153EDD3778559E CRC64;
Query Match 58.1%; Score 43; DB 2; Length 416;
Best Local Similarity 69.2%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOQTQQATT 14
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Db 63 NNVLIPLEQQPTT 75

RESULT 8
Q5X3U5 LEGPA
ID Q5X3U5 LEGPA PRELIMINARY; PRT; 417 AA.
AC Q5X3U5;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
GN OrderedLocusNames=lp1939;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazaleat C., Rusnikoff C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaeser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
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CC -----
DR EMBL; CR628336; CAH13091.1; -; Genomic_DNA.
KW Legiolysin; lpp1939; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 417 AA; 49131 MW; 01F68A54B430C7E2 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 417;
Best Local Similarity 69.2%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOQTQQATT 14
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Db 63 NNVLIPLEQQPTT 75

RESULT 9
Q5ZU51 LEGPH
ID Q5ZU51 LEGPH PRELIMINARY; PRT; 463 AA.
AC Q5ZU51;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE EbaA protein.
GN OrderedLocusNames=lp91957;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chlen M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Stehenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
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```
RA Segal G., Ou X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Ruso J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
CC -----
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CC -----
DR EMBL; AE017354; AAU28026.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 463 AA; 54449 MW; BE76CBED5D81D264 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 463;
Best Local Similarity 69.2%; Pred. No. 34;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOQTQQATT 14
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Db 87 NNVLIPLEQQPTT 99

RESULT 10
Q7R036 GIALA
ID Q7R036 GIALA PRELIMINARY; PRT; 505 AA.
AC Q7R036;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE GLP 456 18539 20056.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AACB01000038; EAA40651.1; -; Genomic_DNA.
DR InterPro; IPR003198; Amidino trans.
DR Pfam; PF02274; Amidinotransf; 1.
SQ SEQUENCE 505 AA; 55735 MW; 99E2CBF5B56824B0 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 505;
Best Local Similarity 57.1%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNVLIOQTQQATT 15
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Db 93 NNVMFMRDQQTTR 106

RESULT 11
Q27657 GIALA
ID Q27657 GIALA PRELIMINARY; PRT; 580 AA.
AC Q27657;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Arginine deiminase (EC 3.5.3.6).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
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RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Portland 1;  
 RX MEDLINE=98136144; PubMed=9468500; DOI=10.1074/jbc.273.8.4470;  
 RA Knodler L.A., Sekyere E.O., Stewart T.S., Schofield P.J.,  
 RA Edwards M.R.,  
 RT Cloning and expression of a prokaryotic enzyme, arginine deiminase,  
 RT from a primitive eukaryote *Giardia intestinalis*.  
 RL J. Biol. Chem. 273:4470-4477(1998).  
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 CC -----  
 DR EMBL: U49236; AAC06116.1; -; Genomic\_DNA.  
 DR PIR: T45064; T45064.  
 DR BioCyc: MetaCyc:MONOMER-11205; -;  
 DR GO: GO:0016990; F:arginine deiminase activity; IEA.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR InterPro: IPR003198; Amidino trans.  
 DR Pfam: PF02274; Amidinotransf\_1.  
 KW Hydrolase.  
 SQ SEQUENCE 580 AA; 64132 MW; 4812F389D0F5357A CRC64;  
 Query Match 58.1%; Score 43; DB 2; Length 580;  
 Best Local Similarity 57.1%; Pred. No. 44;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 NNVLITDQOATTR 15  
 Db 168 NNVMFMDQITTR 181  
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 ID Q7ZXI4 XENLA PRELIMINARY; PRT; 854 AA.  
 AC Q7ZXI4;  
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2003, sequence version 1.  
 DE MGC52979 protein.  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Heltón E., Kettman M., Madan A., Rodríguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
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 CC -----  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative".  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the AAA ATPase family.  
 CC -----  
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 CC -----  
 DR EMBL: BC044980; AAH44980.1; -; mRNA.  
 DR HSSP: Q01853; IR7R.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0017111; F:nucleoside-triphosphatase activity; IEA.  
 DR GO: GO:0000166; F:nucleotide binding; IEA.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003959; AAA\_ATPase\_cent.  
 DR InterPro: IPR003960; AAA\_sub.  
 DR Pfam: PF00004; AAA; 2.  
 DR SMART: SM00382; AAA; 2.  
 DR PROSITE: PS00674; AAA; 2.  
 KW ATP-binding; Nucleotide-binding.  
 SQ SEQUENCE 854 AA; 93597 MW; F91339E502C41BE3 CRC64;  
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 Best Local Similarity 78.6%; Pred. No. 1.4e+02;  
 Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 Qy 2 NNVLITDQOATTR 14  
 Db 483 NRVLQIKDQOATTR 496  
 RESULT 13  
 ID Q8H475 ORYSA PRELIMINARY; PRT; 106 AA.  
 AC Q8H475;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE Hypothetical protein P0470D12.115.  
 GN Name=P0470D12.115;  
 OS *Oryza sativa* (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;  
 OC Ehrhartoideae; Oryzoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC  
 RT clone:P0470D12".  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
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 DR EMBL: AP004300; BAC15985.1; -; Genomic\_DNA.  
 DR Gramene; Q8H475; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 106 AA; 12281 MW; 8016731B1945298F CRC64;  
 Query Match 55.4%; Score 41; DB 2; Length 106;  
 Best Local Similarity 46.7%; Pred. No. 15;  
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 RNNVLITDQOATTR 15  
 Db 10 RNNGVMELEQATSR 24

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ID Q6FP28_CANGA PRELIMINARY; PRT; 247 AA.
AC Q6FP28;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Similar to sp|P39721 Saccharomyces cerevisiae YAL049C.
GN OrderedLocusNames=CAGL0J071283;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OK NCBI_TaxID=5478;
RN [1]
FN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talia E.,
RA Garbay N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Boffay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bolesame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
FT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
CC -----
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CC -----
DR EMBL; CR380956; CAG60967.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002925; DieneLactn_hydro.
DR Pfam; PF01738; DLH; 1.
KW Complete proteome.
SQ SEQUENCE 247 AA; 27274 MW; AEB540BB8B628D35 CRC64;

Query Match 55.4%; Score 41; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQAT 13
Db 57 NNVLITADQAT 68

RESULT 15
Q4SVF5_TETNG
ID Q4SVF5_TETNG PRELIMINARY; PRT; 260 AA.
AC Q4SVF5;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromosome 7 SCF13760, whole genome shotgun sequence.
GN ORFNames=GSTEN00012005001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OK NCBI_TaxID=99883;
RN [1]
FN NUCLEOTIDE SEQUENCE.
RP PubMed=15496914; DOI=10.1038/nature03025;
RX PubMed=15496914; DOI=10.1038/nature03025;

Jailon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
Maucler E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
FN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC -----
DR EMBL; CAE01013760; CAF95377.1; -; Genomic DNA.
SQ SEQUENCE 260 AA; 28404 MW; 7E3DC627AF6D41A2 CRC64;

Query Match 55.4%; Score 41; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NNVLITDQAT 11
Db 69 NNVLITADQAT 78

Search completed: August 30, 2006, 04:29:21
Job time : 61.4848 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 14.8485 Seconds  
(without alignments)  
88.424 Million cell updates/sec

Title: US-10-758-165a-3

Perfect score: 74

Sequence: 1 RNNVLQTDQQAATTR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pep.\*
  - 2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pep.\*
  - 3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pep.\*
  - 4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H COMB.pep.\*
  - 5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.\*
  - 6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pep.\*
  - 7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	58.1	580	2	US-09-723-546-10
2	41	55.4	108	2	US-09-281-760E-37
3	41	55.4	312	2	US-09-701-623C-2
4	41	55.4	426	1	US-08-336-583-2
5	41	55.4	426	5	PCT-US95-13795-2
6	38	51.4	345	2	US-09-270-767-41480
7	38	51.4	613	2	US-09-026-001A-10
8	38	51.4	613	2	US-09-986-620-10
9	38	51.4	621	2	US-09-026-001A-18
10	38	51.4	621	2	US-09-996-620-18
11	37	50.0	370	2	US-09-328-352-5826
12	37	50.0	431	2	US-09-479-614-14
13	37	50.0	496	2	US-09-479-614-2
14	37	50.0	496	2	US-09-479-614-29
15	36	48.6	153	2	US-09-248-796A-22386
16	36	48.6	199	2	US-09-107-433-2754
17	36	48.6	383	2	US-09-328-352-5969
18	36	48.6	441	2	US-09-583-110-4400
19	36	48.6	445	2	US-09-107-433-5039
20	36	48.6	447	2	US-09-205-258-408
21	36	48.6	447	2	US-10-004-860-408
22	36	48.6	461	2	US-09-991-181-301
23	36	48.6	461	2	US-09-980-444-301
24	36	48.6	461	2	US-09-987-333-301
25	36	48.6	461	2	US-09-992-598-301
26	36	48.6	461	2	US-09-989-735-301

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Sequence 24803, A  
Sequence 1374, Ap  
Sequence 46161, A  
Sequence 4821, Ap  
Sequence 3544, Ap  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 118, App  
Sequence 102, App  
Sequence 15, Appl  
Sequence 12964, A  
Sequence 5521, Ap

ALIGNMENTS

RESULT 1

US-09-723-546-10  
; Sequence 10, Application US/09723546  
; Patent No. 6737259  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A  
; TITLE OF INVENTION: Modified Arginine Deiminase  
; FILE REFERENCE: PH080059  
; CURRENT APPLICATION NUMBER: US/09/723,546  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/023,809  
; PRIOR FILING DATE: 1998-02-13  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 580  
; TYPE: PRT  
; ORGANISM: Qiardia intestinalis  
US-09-723-546-10

Query Match 58.1%; Score 43; DB 2; Length 580;  
Best Local Similarity 57.1%; Pred. No. 14;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNVLIQTDQQAATTR 15  
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Db 168 NNVFVRDQQTTR 181

RESULT 2

US-09-281-760E-37  
; Sequence 37, Application US/09281760E  
; Patent No. 6734287  
; GENERAL INFORMATION:  
; APPLICANT: Lawton, Robert  
; APPLICANT: Mermer, Brion  
; APPLICANT: Francoeur, Greg  
; TITLE OF INVENTION: Specific Binding Protein for Treating  
; TITLE OF INVENTION: Canine Allergy  
; FILE REFERENCE: 01-1275A  
; CURRENT APPLICATION NUMBER: US/09/281,760E  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: 09/058,331  
; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 108  
; TYPE: PRT

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; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (460)..(462)
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; FEATURE:
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; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
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; OTHER INFORMATION: "n" stands for any nucleic acid
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Query Match 55.4%; Score 41; DB 2; Length 108;
Best Local Similarity 64.3%; Pred. No. 4.7;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 RNNVLIQTDOQATT 14
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Db 43 RNDSPITQDQYTTT 56
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RESULT 3
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2
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Query Match 55.4%; Score 41; DB 2; Length 312;
Best Local Similarity 64.3%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 RNNVLIQTDOQATT 14
||: ||||| ||
Db 255 RNDSPITQDQYTTT 268
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RESULT 4
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2
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Query Match 55.4%; Score 41; DB 1; Length 426;
Best Local Similarity 64.3%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 RNNVLIQTDOQATT 14
||: ||||| ||
Db 357 RNDSPITQDQYTTT 370
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RESULT 5  
PCT-US95-13795-2  
; Sequence 2, Application PC/TUS9513795  
; GENERAL INFORMATION:  
; APPLICANT: HOLLIS, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13795  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E.  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19211Y  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-6734  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-13795-2

Query Match 55.4%; Score 41; DB 5; Length 426;  
Best Local Similarity 64.3%; Pred. No. 23;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14  
||:|||||  
Db 357 RNDSPITQDQYTT 370

RESULT 6  
US-09-270-767-41480  
; Sequence 41480, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41480  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: *Drosophila melanogaster*  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-41480

Query Match 51.4%; Score 38; DB 2; Length 345;  
Best Local Similarity 57.1%; Pred. No. 63;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RNNVLIQTDDQATT 15  
||:|||||  
Db 77 NOKLIRKNOQTTR 90  
RESULT 7  
US-09-026-001A-10  
; Sequence 10, Application US/09026001A  
; Patent No. 6413760  
; GENERAL INFORMATION:  
; APPLICANT: Boodhoo, Anechand  
; APPLICANT: Seehra, Jasbir  
; APPLICANT: Shaw, Gray  
; APPLICANT: Sako, Dianne  
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,001A  
; FILING DATE: 18-FEB-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: G15293B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 613 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-026-001A-10

Query Match 51.4%; Score 38; DB 2; Length 613;  
Best Local Similarity 53.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQAT 13  
||:|||||  
Db 261 RNEINVQSDVQAT 273

RESULT 8  
US-09-996-620-10  
; Sequence 10, Application US/09996620  
; Patent No. 6881404  
; GENERAL INFORMATION:  
; APPLICANT: Boodhoo, Anechand  
; APPLICANT: Seehra, Jasbir  
; APPLICANT: Shaw, Gray  
; APPLICANT: Sako, Dianne  
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
; PROTEASE, POLYNUCLEOTIDES ENCODING SAME AND RELATED PROTEAS  
; THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.

;; STREET: 87 CambridgePark Drive  
;; CITY: Cambridge  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02140  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/996,620  
;; FILING DATE: 27-Feb-1998  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: 09/026,001  
;; FILING DATE: 18-FEB-1998  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Brown, Scott A.  
;; REGISTRATION NUMBER: 32,724  
;; REFERENCE/DOCKET NUMBER: G15293B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 498-8224  
;; TELEFAX: (617) 876-5851  
;;  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 613 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-996-620-10  
;  
Query Match 51.4%; Score 38; DB 2; Length 613;  
Best Local Similarity 53.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
;  
Qy 1 RNNVLQTDQQT 13  
||:|:|:|  
Db 261 RNEINVQSDVQT 273  
;  
RESULT 9  
US-09-026-001A-18  
; Sequence 18, Application US/09026001A  
; Patent No. 6413760  
; GENERAL INFORMATION:  
; APPLICANT: Boodhoo, Amechand  
; APPLICANT: Seehra, Jasbir  
; APPLICANT: Shaw, Gray  
; APPLICANT: Sako, Dianne  
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,001A  
; FILING DATE: 18-FEB-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.

;; REGISTRATION NUMBER: 32,724  
;; REFERENCE/DOCKET NUMBER: G15293B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 498-8224  
;; TELEFAX: (617) 876-5851  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 621 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-026-001A-18  
;  
Query Match 51.4%; Score 38; DB 2; Length 621;  
Best Local Similarity 53.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
;  
Qy 1 RNNVLQTDQQT 13  
||:|:|:|  
Db 269 RNEINVQSDVQT 281  
;  
RESULT 10  
US-09-996-620-18  
; Sequence 18, Application US/09996620  
; Patent No. 6881404  
; GENERAL INFORMATION:  
; APPLICANT: Boodhoo, Amechand  
; APPLICANT: Seehra, Jasbir  
; APPLICANT: Shaw, Gray  
; APPLICANT: Sako, Dianne  
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/996,620  
; FILING DATE: 27-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 09/026,001  
; FILING DATE: 18-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: G15293B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 621 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-996-620-18  
;  
Query Match 51.4%; Score 38; DB 2; Length 621;



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Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 13
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Db 269 RNEINVQSDVQAT 281

RESULT 11
US-09-328-352-5826
; Sequence 5826, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5826
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5826

Query Match 50.0%; Score 37; DB 2; Length 370;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
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Db 175 KNNIVYTTDSATS 188

RESULT 12
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 50.0%; Score 37; DB 2; Length 431;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLITDQQATT 14
   | : : || : ||
Db 363 NDSFVRTEQQATT 375

RESULT 13
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
```

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FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLITDQQATT 14
   | : : || : ||
Db 428 NDSFVRTEQQATT 440

RESULT 14
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLITDQQATT 14
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Db 428 NDSFVRTEQQATT 440

RESULT 15
US-09-248-796A-22386
; Sequence 22386, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22386
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22386
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Query Match 48.6%; Score 36; DB 2; Length 153;  
Best Local Similarity 77.8%; Pred. No. 57;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNNVLIQTD 9  
||| |||  
Db 21 RNNYFIQTD 29

Search completed: August 30, 2006, 04:33:03  
Job time : 15.8485 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 75.7576 Seconds  
(without alignments)  
91.717 Million cell updates/sec

Title: US-10-758-165a-3

Perfect score: 74

Sequence: 1 RNNVLIQTDDQATTR 15

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Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.Main.\*

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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	US-10-758-165-3	Sequence 3, Appli
2	74	100.0	424	US-10-451-078-2	Sequence 2, Appli
3	74	100.0	424	US-10-451-078-4	Sequence 4, Appli
4	74	100.0	569	US-10-214-524-30	Sequence 30, Appli
5	49	66.2	15	US-10-052-788-4	Sequence 4, Appli
6	43	58.1	580	US-10-674-666-17	Sequence 17, Appli
7	43	58.1	580	US-10-757-843-10	Sequence 10, Appli
8	41.5	56.1	854	US-10-732-923-23294	Sequence 23294, A
9	41	55.4	15	US-10-758-165-1	Sequence 1, Appli
10	41	55.4	105	US-10-437-963-129557	Sequence 129557,
11	41	55.4	312	US-10-369-493-6713	Sequence 6713, Ap
12	41	55.4	312	US-10-723-207-2	Sequence 2, Appli
13	41	55.4	426	US-10-214-524-28	Sequence 28, Appli
14	41	55.4	917	US-10-437-963-181484	Sequence 181484,
15	40	54.1	15	US-10-758-165-7	Sequence 7, Appli
16	40	54.1	567	US-10-214-524-33	Sequence 33, Appli
17	38	51.4	558	US-10-437-963-185049	Sequence 185049,
18	38	51.4	613	US-09-996-620-10	Sequence 10, Appli
19	38	51.4	613	US-11-066-236-10	Sequence 10, Appli
20	38	51.4	621	US-09-996-620-18	Sequence 18, Appli
21	38	51.4	621	US-11-066-236-18	Sequence 18, Appli
22	38	51.4	703	US-10-282-122A-72382	Sequence 72382, A
23	38	51.4	814	US-10-128-714-8100	Sequence 8100, Ap
24	38	51.4	902	US-11-188-298-12745	Sequence 12745, A
25	38	51.4	1827	US-11-057-058-62	Sequence 62, Appli
26	37	50.0	15	US-10-758-165-2	Sequence 2, Appli
27	37	50.0	67	US-10-437-963-138338	Sequence 138338,

28 37 50.0 223 4 US-10-389-566-587 Sequence 587, Appli  
29 37 50.0 431 3 US-09-479-614-14 Sequence 14, Appli  
30 37 50.0 431 4 US-10-409-772-14 Sequence 14, Appli  
31 37 50.0 496 3 US-09-479-614-2 Sequence 2, Appli  
32 37 50.0 496 3 US-09-479-614-29 Sequence 29, Appli  
33 37 50.0 496 4 US-10-214-524-25 Sequence 25, Appli  
34 37 50.0 496 4 US-10-409-772-2 Sequence 2, Appli  
35 37 50.0 496 4 US-10-409-772-29 Sequence 29, Appli  
36 37 50.0 663 4 US-10-389-566-1053 Sequence 1053, Ap  
37 37 50.0 663 5 US-10-732-923-9730 Sequence 9730, Ap  
38 37 50.0 750 4 US-10-425-115-351098 Sequence 351098,  
39 36.5 49.3 272 4 US-10-425-115-233903 Sequence 233903,  
40 36 48.6 21 4 US-10-340-288-37 Sequence 37, Appli  
41 36 48.6 143 4 US-10-128-714-8304 Sequence 8304, Ap  
42 36 48.6 199 4 US-10-425-115-299967 Sequence 299967,  
43 36 48.6 199 5 US-10-617-320-2754 Sequence 2754, Ap  
44 36 48.6 309 4 US-10-264-237-2751 Sequence 2751, Ap  
45 36 48.6 318 4 US-10-128-714-3304 Sequence 3304, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-758-165-3

; Sequence 3, Application US/10758165

; Publication No. US20050196816A1

; GENERAL INFORMATION:

; APPLICANT: Hammerberg, Bruce

; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

; FILE REFERENCE: 5051-661

; CURRENT APPLICATION NUMBER: US/10758,165

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: US 60/440,472

; PRIOR FILING DATE: 2003-01-16

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Equus caballus

US-10-758-165-3

Query Match

Best Local Similarity 100.0%; Score 74; DB 5; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15

Db 1 RNNVLIQTDDQATTR 15

##### RESULT 2

US-10-451-078-2

; Sequence 2, Application US/10451078

; Publication No. US20040115764A1

; GENERAL INFORMATION:

; APPLICANT: Leibold, Wolfgang

; APPLICANT: Bettina, Wagner

; APPLICANT: Radbruch, Andreas

; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the Heavy Chain of an Equine IGE Allotype, Recombinant

; TITLE OF INVENTION: Heavy Chain of an Equine IGE Allotype, Recombinant

; TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding

; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use

; FILE REFERENCE: 0310017aa

; CURRENT APPLICATION NUMBER: US/10/451,078

; CURRENT FILING DATE: 2003-12-24

; PRIOR APPLICATION NUMBER: PCT/DE01/04810

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: DE 100 64 415.5

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Equus caballus
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (1)..(97)
; OTHER INFORMATION: CH1 domain, IgE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (98)..(205)
; OTHER INFORMATION: CH2 domain, IgE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (206)..(312)
; OTHER INFORMATION: CH3 domain, IgE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (313)..(424)
; OTHER INFORMATION: CH4 domain, IgE allotype a
; US-10-451-078-2

Query Match      100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
Db 356 RNNVLIQTDDQATTR 370

RESULT 3
US-10-451-078-4
; Sequence 4, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bettina, Wagner
; APPLICANT: Radbruch, Andreas
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
; TITLE OF INVENTION: Heavy Chain of an Equine IgE Allotype, Recombinant
; TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 03100177aa
; CURRENT APPLICATION NUMBER: US/10/451,078
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Equus caballus
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (1)..(97)
; OTHER INFORMATION: CH1 domain, IgE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (98)..(205)
; OTHER INFORMATION: CH2 domain, IgE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (206)..(312)
; OTHER INFORMATION: CH3 domain, IgE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (313)..(424)
; OTHER INFORMATION: CH4 domain, IgE allotype b
; US-10-451-078-4
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Query Match      100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
Db 356 RNNVLIQTDDQATTR 370

RESULT 4
US-10-214-524-30
; Sequence 30, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Horse (Equus caballus)
; US-10-214-524-30
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Query Match      100.0%; Score 74; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
Db 501 RNNVLIQTDDQATTR 515
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RESULT 5
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; TITLE OF INVENTION: Induction of Anti-IgE Antibodies
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
; OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon
; OTHER INFORMATION: heavy chain
; US-10-052-788-4
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Query Match      66.2%; Score 49; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IQTDDQATTR 15
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Db      1 IOTDQQAATR 10
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RESULT 6
US-10-674-666-17
; Sequence 17, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-674-666-17
Query Match      58.1%; Score 43; DB 4; Length 580;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 NNVLQTDQQAATR 15
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Db      168 NNVFMRDQQAITR 181

RESULT 7
US-10-757-843-10
; Sequence 10, Application US/10757843
; Publication No. US20050129706A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT APPLICATION NUMBER: US/10/757,843
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/723,546
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 10
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-757-843-10
Query Match      58.1%; Score 43; DB 5; Length 580;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 NNVLQTDQQAATR 15
|||: ||| |||
Db      168 NNVFMRDQQAITR 181

RESULT 8
US-10-732-923-23294
; Sequence 23294, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
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; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 23294
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-23294
Query Match      56.1%; Score 41.5; DB 5; Length 854;
Best Local Similarity 78.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      2 NNVLQTDQQAATR 14
| ||| ||| |||
Db      483 NRVLQIKDQQAATT 496

RESULT 9
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1
Query Match      55.4%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLQTDQQAATT 14
||: ||| |||
Db      1 RNDSPITDQQAATT 14

RESULT 10
US-10-437-963-129557
; Sequence 129557, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 129557
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31803C.1.pep
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US-10-437-963-129557

Query Match 55.4%; Score 41; DB 4; Length 105;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15  
||| : : : ||| : |  
Db 10 RNNGVMELEEQATSR 24

RESULT 11

US-10-369-493-6713  
; Sequence 6713, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6713  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6713

Query Match 55.4%; Score 41; DB 4; Length 312;  
Best Local Similarity 57.1%; Pred. No. 67;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQDQATTR 15  
: ||| : : : |  
Db 159 DNVLQKDEENTAR 172

RESULT 12

US-10-723-207-2  
; Sequence 2, Application US/10723207  
; Publication No. US20050250934A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Wafield, Alan M.  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; TITLE OF INVENTION: ALLERGY  
; FILE REFERENCE: 1151-4153US2  
; CURRENT APPLICATION NUMBER: US/10/723,207  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: 09/701,623  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Dog  
; FEATURE:  
; OTHER INFORMATION: CH2CH3n of dog IgE  
; PUBLICATION INFORMATION:  
; AUTHORS: Patel,  
; JOURNAL: Immunogenetics

; VOLUME: 41  
; PAGES: 282-286  
; DATE: 1995  
US-10-723-207-2

Query Match 55.4%; Score 41; DB 5; Length 312;  
Best Local Similarity 64.3%; Pred. No. 67;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTT 14  
||: ||||| ||  
Db 255 RNDSPITQDQYTTT 268

RESULT 13

US-10-214-524-28  
; Sequence 28, Application US/10214524  
; Publication No. US20030073142A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Swei-Shen Alex  
; APPLICANT: Yang, Yong-Min  
; APPLICANT: Barankiewicz, Theresa J.  
; APPLICANT: Chen, Zhong  
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
; FILE REFERENCE: IGE-00101.P.1.1  
; CURRENT APPLICATION NUMBER: US/10/214,524  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/312,120  
; PRIOR FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Dog (Canis familiaris)  
US-10-214-524-28

Query Match 55.4%; Score 41; DB 4; Length 426;  
Best Local Similarity 64.3%; Pred. No. 95;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTT 14  
||: ||||| ||  
Db 357 RNDSPITQDQYTTT 370

RESULT 14

US-10-437-963-181484  
; Sequence 181484, Application US/10437963.  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 181484  
; LENGTH: 917  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(917)  
; OTHER INFORMATION: unsure at all Xaa locations

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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78753C.1.pep
US-10-437-963-181484

Query Match      55.4%; Score 41; DB 4; Length 917;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
Db 143 RNNIMVILDNQMTT 156

RESULT 15
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: S651-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match      54.1%; Score 40; DB 5; Length 15;
Best Local Similarity 46.7%; Pred. No. 3.3;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 15
Db 1 RNDAPVQADRHSTTR 15
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Search completed: August 30, 2006, 05:13:02  
Job time : 76.7576 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 7.72727 Seconds  
(without alignments)  
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Title: US-10-758-165a-3

Perfect score: 74

Sequence: 1 RNNVLIQTDDQATT 15

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Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.psp:\*\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.psp:\*\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.psp:\*\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.psp:\*\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.psp:\*\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.psp:\*\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.psp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	51.4	554	6	US-10-449-902-40987 Sequence 40987, A
2	36	48.6	348	7	US-11-197-712-247 Sequence 247, App
3	36	48.6	585	7	US-11-330-403-2292 Sequence 2292, Ap
4	35	47.3	223	6	US-10-953-349-1194 Sequence 1194, Ap
5	35	47.3	223	7	US-11-056-355B-23703 Sequence 23703, A
6	35	47.3	240	6	US-10-953-349-1098 Sequence 1098, Ap
7	35	47.3	240	7	US-11-056-355B-43157 Sequence 43157, A
8	35	47.3	240	7	US-11-056-355B-85177 Sequence 85177, A
9	35	47.3	317	6	US-10-953-349-1193 Sequence 1193, Ap
10	35	47.3	317	7	US-11-056-355B-23702 Sequence 23702, A
11	35	47.3	388	6	US-10-953-349-1192 Sequence 1192, Ap
12	35	47.3	388	7	US-11-056-355B-23701 Sequence 23701, A
13	35	47.3	409	6	US-10-953-349-1097 Sequence 1097, Ap
14	35	47.3	409	7	US-11-056-355B-43156 Sequence 43156, A
15	35	47.3	409	7	US-11-056-355B-85176 Sequence 85176, A
16	35	47.3	498	6	US-10-953-349-37842 Sequence 37842, A
17	35	47.3	578	6	US-10-953-349-37841 Sequence 37841, A
18	35	47.3	634	6	US-10-953-349-37840 Sequence 37840, A
19	35	47.3	825	7	US-11-330-403-2887 Sequence 2887, Ap
20	34	45.9	257	7	US-11-056-355B-18603 Sequence 18603, A
21	34	45.9	358	6	US-10-953-349-4802 Sequence 4802, Ap
22	34	45.9	358	7	US-11-056-355B-27751 Sequence 27751, A
23	34	45.9	358	7	US-11-056-355B-31341 Sequence 31341, A
24	34	45.9	358	7	US-11-056-355B-105308 Sequence 105308, A
25	34	45.9	358	7	US-11-056-355B-116547 Sequence 116547, A

#### ALIGNMENTS

##### RESULT 1

US-10-449-902-40987  
; Sequence 40987, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40987  
; LENGTH: 554  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-40987

Query Match 51.4% Score 38; DB 6; Length 554;  
Best Local Similarity 42.9%; Pred. No. 30;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14  
Db 144 KNNIMVLDNQMTT 157

##### RESULT 2

US-11-197-712-247  
; Sequence 247, Application US/11197712  
; Publication No. US20060130160A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Bougueret, Lydie  
; APPLICANT: Jobert, Severin  
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS  
; FILE REFERENCE: 78 USA CIP  
; CURRENT APPLICATION NUMBER: US/11/197,712  
; CURRENT FILING DATE: 2005-08-04  
; PRIOR APPLICATION NUMBER: US/03/876,997  
; PRIOR FILING DATE: 2001-06-08

26 34 45.9 366 7 US-11-056-355B-71337 Sequence 71337, A  
27 34 45.9 372 7 US-11-056-355B-71336 Sequence 71336, A  
28 34 45.9 373 7 US-11-293-697-2882 Sequence 2882, Ap  
29 34 45.9 411 7 US-11-056-355B-69409 Sequence 69409, A  
30 34 45.9 411 7 US-11-056-355B-69694 Sequence 69694, A  
31 34 45.9 414 7 US-11-056-355B-71537 Sequence 71537, A  
32 34 45.9 414 7 US-11-056-355B-86118 Sequence 86118, A  
33 34 45.9 417 7 US-11-056-355B-69408 Sequence 69408, A  
34 34 45.9 417 7 US-11-056-355B-71335 Sequence 71335, A  
35 34 45.9 430 7 US-11-056-355B-69693 Sequence 69693, A  
36 34 45.9 430 7 US-11-056-355B-72244 Sequence 72244, A  
37 34 45.9 440 7 US-11-056-355B-71536 Sequence 71536, A  
38 34 45.9 440 7 US-11-056-355B-86117 Sequence 86117, A  
39 34 45.9 452 7 US-11-056-355B-72243 Sequence 72243, A  
40 34 45.9 466 7 US-11-056-355B-69407 Sequence 69407, A  
41 34 45.9 466 7 US-11-056-355B-72242 Sequence 72242, A  
42 34 45.9 502 7 US-11-293-697-3735 Sequence 3735, Ap  
43 34 45.9 558 7 US-11-056-355B-17556 Sequence 17556, A  
44 34 45.9 573 7 US-11-056-355B-71535 Sequence 71535, A  
45 34 45.9 576 7 US-11-056-355B-86116 Sequence 86116, A

;; PRIOR APPLICATION NUMBER: US 09/731,872  
;; PRIOR FILING DATE: 2000-12-07  
;; PRIOR APPLICATION NUMBER: US 60/187,470  
;; PRIOR FILING DATE: 2000-03-06  
;; PRIOR APPLICATION NUMBER: US 60/169,629  
;; PRIOR FILING DATE: 1999-12-08  
;; NUMBER OF SEQ ID NOS: 482  
;; SOFTWARE: Patent.pm  
; SEQ ID NO 247  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -29...-1  
US-11-197-712-247

Query Match 48.6%; Score 36; DB 7; Length 348;  
Best Local Similarity 53.8%; Pred. No. 42;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 NVLIQTQQATRR 15  
| | | | |  
Db 175 NVVETDQIMVR 187

RESULT 3  
US-11-330-403-2292  
; Sequence 2292, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 2292  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea 70-15  
US-11-330-403-2292

Query Match 48.6%; Score 36; DB 7; Length 585;  
Best Local Similarity 75.0%; Pred. No. 77;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NNVLQTD 9  
| | | | |  
Db 243 NNVLVEID 250

RESULT 4  
US-10-953-349-1194  
; Sequence 1194, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1194  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-1194

Query Match 47.3%; Score 35; DB 6; Length 223;  
Best Local Similarity 50.0%; Pred. No. 39;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 RNNVLIQTQQATT 14  
| | | | |  
Db 195 RQNVVVELVQAATT 208

RESULT 5  
US-11-056-355B-23703  
; Sequence 23703, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 23703  
; LENGTH: 223  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(223)  
; OTHER INFORMATION: Ceres Seq. ID no. 13487886  
US-11-056-355B-23703

Query Match 47.3%; Score 35; DB 7; Length 223;  
Best Local Similarity 50.0%; Pred. No. 39;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTQQATT 14  
| | | | |  
Db 195 RQNVVVELVQAATT 208

RESULT 6  
US-10-953-349-1098  
; Sequence 1098, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1098  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-1098

Query Match 47.3%; Score 35; DB 6; Length 240;  
Best Local Similarity 38.5%; Pred. No. 42;  
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLQTDQQAATT 14  
| | | | |  
Db 11 NNVLKLDQAATS 23

RESULT 7  
US-11-056-355B-43157  
; Sequence 43157, Application US/11056355B  
; Publication No. US20060150283A1

```
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 43157
; LENGTH: 240
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(240)
; OTHER INFORMATION: Ceres Seq. ID no. 13487787
US-11-056-355B-43157

Query Match      47.3%; Score 35; DB 7; Length 240;
Best Local Similarity 38.5%; Pred. No. 42;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      2 NNVLITDQQAATT 14
Db      11 NNVLKLDQASTS 23

RESULT 8
US-11-056-355B-85177
; Sequence 85177, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 85177
; LENGTH: 240
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(240)
; OTHER INFORMATION: Ceres Seq. ID no. 12679238
US-11-056-355B-85177

Query Match      47.3%; Score 35; DB 7; Length 240;
Best Local Similarity 38.5%; Pred. No. 42;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      2 NNVLITDQQAATT 14
Db      11 NNVLKLDQASTS 23

RESULT 9
US-10-953-349-1193
; Sequence 1193, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
```

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; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1193
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1193

Query Match      47.3%; Score 35; DB 6; Length 317;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLITDQQAATT 14
Db      289 RQNVVVELVQAATT 302

RESULT 10
US-11-056-355B-23702
; Sequence 23702, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 23702
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 13487885
US-11-056-355B-23702

Query Match      47.3%; Score 35; DB 7; Length 317;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLITDQQAATT 14
Db      289 RQNVVVELVQAATT 302

RESULT 11
US-10-953-349-1192
; Sequence 1192, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1192
; LENGTH: 388
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1192

Query Match      47.3%; Score 35; DB 6; Length 388;
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Best Local Similarity 50.0%; Pred. No. 74;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLITDQQAATT 14  
| | | | |  
Db 360 RQNVVVELVQAATT 373

## RESULT 12

US-11-056-355B-23701  
; Sequence 23701, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 23701  
; LENGTH: 388  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(388)  
; OTHER INFORMATION: Ceres Seq. ID no. 13487884  
US-11-056-355B-23701

Query Match 47.3%; Score 35; DB 7; Length 388;  
Best Local Similarity 50.0%; Pred. No. 74;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLITDQQAATT 14  
| | | | |  
Db 360 RQNVVVELVQAATT 373

## RESULT 13

US-10-953-349-1097  
; Sequence 1097, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1097  
; LENGTH: 409  
; TYPE: PRP  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-1097

Query Match 47.3%; Score 35; DB 6; Length 409;  
Best Local Similarity 38.5%; Pred. No. 79;  
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RNNVLITDQQAATT 14  
| | | | |  
Db 180 RNNVLKLDQAATS 192

## RESULT 14

US-11-056-355B-43156  
; Sequence 43156, Application US/11056355B

; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 43156  
; LENGTH: 409  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(409)  
; OTHER INFORMATION: Ceres Seq. ID no. 13487786  
US-11-056-355B-43156

Query Match 47.3%; Score 35; DB 7; Length 409;  
Best Local Similarity 38.5%; Pred. No. 79;  
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RNNVLITDQQAATT 14  
| | | | |  
Db 180 RNNVLKLDQAATS 192

## RESULT 15

US-11-056-355B-85176  
; Sequence 85176, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 85176  
; LENGTH: 409  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(409)  
; OTHER INFORMATION: Ceres Seq. ID no. 12679237  
US-11-056-355B-85176

Query Match 47.3%; Score 35; DB 7; Length 409;  
Best Local Similarity 38.5%; Pred. No. 79;  
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RNNVLITDQQAATT 14  
| | | | |  
Db 180 RNNVLKLDQAATS 192

Search completed: August 30, 2006, 04:35:58  
Job time : 7.72727 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 65.4545 Seconds  
(without alignments)  
125.735 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGQKATNIPFYTAPGK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	97	100.0	18	ADRI0609	Dog IgE e
2	97	100.0	312	AA779995	Aay79995 Dog Immun
3	97	100.0	417	AAW23067	Canine Ig
4	97	100.0	426	AAW37753	Canine Ig
5	97	100.0	426	ABP96583	Dog IgE h
6	87	89.7	18	ADRI0610	Cat IgE e
7	87	89.7	431	ADG73237	Cat Immun
8	87	89.7	496	ABP96580	Cat IgE h
9	87	89.7	496	ABU09338	Feline Ig
10	87	89.7	496	ABU09336	Feline Ig
11	87	89.7	496	ADG73251	Cat parti
12	87	89.7	496	ADG73225	Cat parti
13	73	75.3	577	ABP96584	Duckbille
14	68	70.1	343	ABU06204	Platypus
15	58	59.8	337	ADP90022	Opossum-r
16	58	59.8	337	ADN00643	Oro prote
17	58	59.8	338	ADP90025	Opossum-h
18	58	59.8	338	ADN00646	OSO prote
19	58	59.8	341	ABU06206	Immunogen
20	58	59.8	341	ABU03644	Opossum I
21	58	59.8	341	ABU06208	Immunogen
22	58	59.8	342	ABU06205	Immunogen
23	58	59.8	345	ABU06207	Immunogen

24	58	59.8	347	8	ADF90033	Opossum-h
25	58	59.8	347	8	ADN00654	OSO-H pro
26	58	59.8	353	8	ADN00661	H-OCO-H p
27	58	59.8	427	6	ABP96591	Brushtail
28	58	59.8	446	6	ABP96587	Opossum I
29	58	59.8	555	8	ADF90027	Opossum-r
30	58	59.8	555	8	ADN00648	ORORO pro
31	58	59.8	557	8	ADF90031	Opossum-h
32	58	59.8	557	8	ADF90035	Opossum-h
33	58	59.8	557	8	ADN00656	OSO pro
34	58	59.8	557	8	ADN00652	modOSO
35	58	59.8	566	8	ADF90029	Opossum-h
36	58	59.8	566	8	ADF90037	Opossum-h
37	58	59.8	566	8	ADN00658	OSO-H p
38	58	59.8	566	8	ADN00650	modOSO
39	55	56.7	18	8	ADRI0612	Sheep IgE
40	55	56.7	567	6	ABP96588	Pig IgE h
41	53	54.6	341	3	AAU06202	Immunogen
42	53	54.6	342	3	AAU06201	Immunogen
43	46	47.4	135	2	AAU76530	Human ova
44	46	47.4	135	7	ABO81258	Pseudomon
45	46	47.4	386	8	ADU00341	Iron hydr

ALIGNMENTS

RESULT 1	ADRI0609	ADRI0609 standard; peptide; 18 AA.
ID	ADRI0609	
XX	ADRI0609;	
AC	ADRI0609;	
XX	ADRI0609;	
DT	21-OCT-2004	(first entry)
XX	Dog IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.	
DE	Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;	
XX	anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.	
KW	Canis familiaris.	
XX	WO2004065936-A2.	
XX	05-AUG-2004.	
PD	15-JAN-2004; 2004WO-US003566.	
XX	16-JAN-2003; 2003US-0440472P.	
PR	(UYNC-) UNIV NORTH CAROLINA STATE.	
XX	Hammerberg B;	
PI	WPI; 2004-593545/57.	
XX	Novel antibody that specifically binds to mammalian IgE epitope, useful	
PT	for testing an allergen reactivity of IgE sample, detecting mammalian IgE	
PT	or treating asthma or anaphylactic shock.	
XX	Example 6; Page 9; 14pp; English.	
PS	The present invention relates to a novel monoclonal antibody (I) that	
XX	specifically binds to a mammalian IgE epitope, where the epitope is	
CC	between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.	
CC	(I) is useful for testing an allergen reactivity of an IgE sample. The	
CC	allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut	
CC	and corn allergens. The sample is a biological sample collected from a	
CC	dog, cat or horse. (I) is also useful for detecting mammalian IgE and for	
CC	treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal	
CC	antibodies recognise epitopes on canine IgE corresponding to amino acid	
CC	residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the	
CC	canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from	

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTPAGTK 18  
 |||||  
 DB 1 VDGQKATNIPFYTPAGTK 18

RESULT 2  
 AAY79995  
 ID AAY79995 standard; protein; 312 AA.

XX AC AAY79995;

XX XX  
 DT 15-MAY-2000 (first entry)

DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Canis sp.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNB1-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 for immunization against allergy.

XX Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 312 AA;

Query Match 100.0%; Score 97; DB 3; Length 312;

Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VDGQKATNIPFYTPAGTK 18  
 |||||  
 DB 48 VDGQKATNIPFYTPAGTK 65

RESULT 3  
 AAW23067  
 ID AAW23067 standard; protein; 417 AA.

XX AC AAW23067;

XX 30-JUN-2005 (revised)

DT 16-JUN-2005 (revised)

DT 19-FEB-1998 (first entry)

DE Canine IgE heavy chain constant region (exon 1-4 product).

XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX OS Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEXX LAB INC.

XX Mermer B, Harris RA, Siefring AE;

XX WPI; 1997-425031/39.

DR N-PSDB; AAT79278.

XX Isolated canine IgE heavy chain constant region DNA - useful to develop  
 products for treatment of canine allergies and for immunomodulation in  
 dogs.

XX Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE  
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat Type I immediate hypersensitivity, and for immunomodulation

```

CC Revised record issued on 30-JUN-2005 : Typo in comments
XX
SQ Sequence 417 AA;

Query Match      100.0%; Score 97; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGPK 18
   |||||
Db 141 VDGQKATNIPFYTAGPK 158

RESULT 4
AAR97753
ID AAR97753 standard; protein; 426 AA.
XX
AC AAR97753;
XX
DT 28-AUG-1996 (first entry)
XX
DE Canine IgE.
XX
KW IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX
OS Canis familiaris.
XX
PN WO9614867-A1.
XX
PD 23-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US013795.
XX
PR 09-NOV-1994; 94US-00336583.
XX
PR 09-NOV-1994; 94US-00336891.
XX
PA (MERI ) MERCK & CO INC.
XX
XX Hollis GF, Patel MD;
XX
DR WPI; 1996-277321/28.
XX
DR N-PSDB; AAT29824.
XX
XX New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX
XX Claim 11; Page 29-30; 49pp; English.
XX
XX The canine IgE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAT29824) obt'd. from a canine liver DNA library. The
CC cloning of the IgE gene allows prodn. of large quantities of recombinant
CC IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IgE antibody generation). Fragments of IgE can be
CC used in vaccines or to prevent IgE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IgE-mediated immune
CC responses
XX
SQ Sequence 426 AA;

Query Match      100.0%; Score 97; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGPK 18
   |||||
Db 146 VDGQKATNIPFYTAGPK 163

RESULT 5
ABP96583
ID ABP96583 standard; protein; 426 AA.

```

```

XX ABP96583;
AC
XX
DT 28-MAY-2003 (first entry)
XX
DE Dog IgE heavy chain amino acid sequence SEQ ID NO:28.
XX
KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
KW immune response; major histocompatibility complex; MHC; immunogenic;
KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KW urticaria hives.
XX
XX Canis familiaris.
OS
XX
PN WO2003015716-A2.
XX
PD 27-FEB-2003.
XX
PF 08-AUG-2002; 2002WO-US026986.
XX
PR 13-AUG-2001; 2001US-0312120P.
XX
XX (IGET-) IGE THERAPEUTICS INC.
PA
XX
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX WPI; 2003-268242/26.
XX
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IgE, by identifying peptide eliciting CTL response to IgE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
PS Example 7; Page 152-154; 187pp; English.
XX
XX The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IgE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IgE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IgE peptides, C1-3 have antiallergic, antiasthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IgE, and in
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IgE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
SQ Sequence 426 AA;

```

```

Query Match      100.0%; Score 97; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGPK 18
   |||||
Db 146 VDGQKATNIPFYTAGPK 163

```

RESULT 6  
 ID ADR10610 standard; peptide; 18 AA.  
 AC ADR10610;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Cat IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.  
 XX  
 KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KW cat.  
 XX  
 OS Felis catus.  
 XX  
 PN WO2004065936-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 15-JAN-2004; 2004WO-US003566.  
 XX  
 PR 16-JAN-2003; 2003US-0440472P.  
 XX  
 PA (UYN-C) UNIV NORTH CAROLINA STATE.  
 XX  
 PI Hammerberg B;  
 XX  
 PS WPI; 2004-593545/57.  
 XX  
 DR Novel antibody that specifically binds to mammalian IgE epitope, useful  
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 PT or treating asthma or anaphylactic shock.  
 XX  
 XX Example 6; Page 9; 14pp; English.  
 XX  
 CC The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IgE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC cat IgE 3.76 recognition site.  
 XX  
 SQ Sequence 18 AA;  
 DE  
 Query Match 89.7%; Score 87; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VDGGKATNIFPYTAPG 16  
 DB 1 VDGGKATNIFPYTAPG 16  
 DE  
 RESULT 7  
 ID ADG73237 standard; protein; 431 AA.  
 XX  
 AC ADG73237;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX

DE Cat immunoglobulin E (IgE) constant region.  
 XX  
 KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;  
 KW immune response; IgE-mediated response; allergy; cat; constant region.  
 XX  
 OS Felis catus.  
 XX  
 PN US2003216565-A1.  
 XX  
 PD 20-NOV-2003.  
 XX  
 PF 07-APR-2003; 2003US-00409772.  
 XX  
 PR 07-JAN-1999; 99US-0115033P.  
 PR 07-JAN-2000; 2000US-00479614.  
 XX  
 PA (MCCA/) MCCALL C.  
 PA (WEBE/) WEBER E.  
 XX  
 PI McCall C, Weber E;  
 XX  
 DR WPI; 2004-010802/01.  
 DR N-PSDB; ADG73236.  
 XX  
 PT New isolated nucleic acid molecule encoding a portion of a feline IgE  
 PT heavy chain protein, useful for treating and/or eliciting feline immune  
 PT responses for IgE-mediated responses, such as allergies.  
 XX  
 PS Claim 12; SEQ ID NO 14; 44pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid molecule (I) encoding a  
 CC portion of a feline IgE heavy chain protein. The methods and compositions  
 CC of the present invention are useful for eliciting feline immune responses  
 CC for and/or treating IgE-mediated responses, such as allergies. This is  
 CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.  
 XX  
 SQ Sequence 431 AA;  
 DE  
 Query Match 89.7%; Score 87; DB 8; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VDGGKATNIFPYTAPG 16  
 DB 151 VDGGKATNIFPYTAPG 166  
 DE  
 RESULT 8  
 ID ABP96580 standard; protein; 496 AA.  
 XX  
 AC ABP96580;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Cat IgE heavy chain amino acid sequence SEQ ID NO:25.  
 XX  
 KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
 KW immune response; major histocompatibility complex; MHC; immunogenic;  
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.  
 XX  
 OS Felis catus.  
 XX  
 PN WO2003015716-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 08-AUG-2002; 2002WO-US026986.  
 XX







RESULT 13  
ABP96584  
ID ABP96584 standard; protein; 577 AA.  
AC ABP96584;  
XX  
DT 28-MAY-2003 (first entry)  
XX  
DE Duckbilled platypus IgE heavy chain amino acid sequence SEQ ID NO:29.  
XX  
XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
KW immune response; major histocompatibility complex; MHC; immunogenic;  
KW anti-allergic; antiallergic; immunosuppressive; vasotropic; cytostatic;  
KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
KW urticaria hives.  
XX  
OS Ornithorhynchus anatinus.  
XX  
PN WO2003015716-A2.  
XX  
XX 27-FEB-2003.  
XX  
PF 08-AUG-2002; 2002WO-US026986.  
XX  
XX 13-AUG-2001; 2001US-0312120P.  
XX  
XX (IGET-) IGE THERAPEUTICS INC.  
XX  
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;  
XX WPI; 2003-268242/26.  
XX  
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
PT against IgE, by identifying peptide eliciting CTL response to IgE  
PT peptides naturally presented by major histocompatibility complex class I  
PT protein.  
XX  
XX Example 7; Page 154-157; 187pp; English.  
XX  
CC The present invention describes a method (M1) for identifying peptides  
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
CC E (IgE), comprising providing a test peptide (T) suspected of being able  
CC to bind to major histocompatibility complex (MHC) class I molecule, and  
CC evaluating (T) for ability to elicit in a mammal a CTL response to  
CC naturally processed and presented IgE peptides, where a peptide that  
CC induces such a response is identified. Also described are compositions:  
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
CC elicit in a mammal a CTL response to naturally processed and presented  
CC IgE peptides. C1-3 have anti-allergic, antiallergic, immunosuppressive,  
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
CC and can be used as inducers of a CTL response against IgE, and in  
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a  
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
CC useful for treating atopic hypersensitivity conditions (such as allergic  
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
CC hives). The present sequence represents an IgE heavy chain amino acid  
CC sequence, which is given in an example from the present invention  
XX  
SQ Sequence 577 AA;  
XX  
Query Match 75.3%; Score 73; DB 6; Length 577;  
Best Local Similarity 86.7%; Pred. No. 0.0026;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
XX  
RESULT 14  
AAB06204  
ID AAB06204 standard; protein; 343 AA.  
AC AAB06204;  
XX  
XX 22-NOV-2000 (first entry)  
XX  
XX Platypus IgE heavy chain constant regions 2, 3 and 4.  
DE  
XX Platypus; immunoglobulin E; IgE; vaccination; infection; allergy; asthma;  
KW eczema; immunogenic peptide.  
XX  
XX Ornithorhynchus anatinus.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 1..343  
FT /label= OTHER  
FT /note= "Xaa=unknown"  
XX  
XX WO2000025722-A2.  
XX  
XX 11-MAY-2000.  
XX  
XX 21-OCT-1999; 99WO-SE001896.  
XX  
XX 02-NOV-1998; 98US-0106652P.  
XX 22-SEP-1999; 99US-00401636.  
XX  
XX (RESI-) RESISTENTIA PHARM AB.  
XX  
XX Hellman LT;  
XX  
XX WPI; 2000-365342/31.  
XX  
XX Immunogenic polypeptides useful for preventing the harmful effects of  
XX immunoglobulin E in mammals.  
XX  
XX Disclosure; Fig 2; 50pp; English.  
XX  
CC The present sequence is an immunogenic peptide consisting of the heavy  
CC chain constant regions 2, 3 and 4 of the platypus IgE. It was used to  
CC construct a number of immunogenic peptides which consisted of regions of  
CC IgE from different mammals, which appear to cause a stronger polyclonal  
CC anti-self IgE response than peptides consisting of the same regions from  
CC one mammal. Immunogenic peptides, particularly those consisting of  
CC different heavy chain constant regions, can be used for vaccination in  
CC humans, against bacterial and viral infections and allergies, such as  
CC asthma, fur, pollen and food allergies and eczema  
XX  
SQ Sequence 343 AA;  
XX  
Query Match 70.1%; Score 68; DB 3; Length 343;  
Best Local Similarity 80.0%; Pred. No. 0.01;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
RESULT 15  
ADF90022  
ID ADF90022 standard; protein; 337 AA.  
XX  
XX ADF90022;  
AC  
XX 26-FEB-2004 (first entry)  
DT

XX Opossum-rat chimeric IgE polypeptide.  
DE  
XX  
XX IGE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;  
KW antiasthmatic; dermatological.  
XX  
XX Chimeric.  
OS Didelphis virginiana.  
OS Rattus sp.  
XX  
XX WO2003096966-A2.  
XX  
XX 27-NOV-2003.  
XX  
XX 15-MAY-2003; 2003WO-IB002503.  
XX  
XX 21-MAY-2002; 2002US-0382552P.  
XX  
XX (RESI-) RESISTENTIA PHARM AB.  
XX  
XX Lundgren M, Fuentes A, Magnusson A;  
PI  
XX  
XX WPI; 2004-042496/04.  
DR N-PSDB; ADF90020, ADF90021.  
XX  
XX New host cell comprising a nucleic acid vector comprising a  
PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or  
PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE  
PT polypeptide.  
XX  
XX Claim 3; SEQ ID NO 3; 23pp; English.  
XX  
XX The present sequence is the protein sequence of an opossum CH2-rat CH3-  
CC opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic  
CC acid encoding ORO can be used for recombinant production of this chimeric  
CC IgE in host, e.g. CHO, cells. The invention provides methods and  
CC materials related to expressing chimeric IgE proteins. Nucleic acid  
CC vectors, host cells, and methods for producing chimeric IgE polypeptides  
CC are provided. When administered to a mammal, the chimeric polypeptides  
CC can reduce the IgE antibody effects of IgE-related diseases such as  
CC asthma, allergies and eczema.  
XX  
XX SQ Sequence 337 AA;  
  
Query Match 59.8%; Score 58; DB 8; Length 337;  
Best Local Similarity 76.9%; Pred. NO. 0.48;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 VDGQKATNIFPYT 13  
| | | | | : | : | | |  
Db 56 VDGQEAENLFPY 68  
  
Search completed: August 30, 2006, 04:22:02  
Job time : 65.4545 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 10.7273 Seconds  
(without alignments)  
161.448 Million cell updates/sec

Title: US-10-758-165a-9  
Perfect score: 97  
Sequence: 1 VDGQKATNIFPYTAPG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR.80.\*  
2: PIR1.\*  
3: PIR2.\*  
4: PIR3.\*  
5: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2 T16880	hypothetical prote
2	46	47.4	579	2 JW0071	asparagine synthas
3	46	47.4	586	2 SE9183	asparagine synthas
4	46	47.4	658	2 AH0110	probable surface p
5	45	46.4	350	2 G95009	sensor histidine k
6	45	46.4	350	2 E97881	histidine kinase (
7	45	46.4	583	1 AJPMN2	asparagine synthas
8	44	45.4	511	2 T16279	hypothetical prote
9	43	44.3	322	2 AD3488	transporter BME18
10	43	44.3	586	1 AJPMN1	asparagine synthas
11	42	43.3	258	2 AF0306	puative trans-acon
12	42	43.3	381	2 AD2436	ATP-binding protei
13	42	43.3	476	2 AC2465	6-phosphogluconate
14	42	43.3	623	2 T21177	hypothetical prote
15	42	43.3	683	2 B71325	conserved hypothet
16	42	43.3	1686	2 A87692	conserved hypothet
17	41	42.3	241	2 T17798	hypothetical prote
18	41	42.3	272	2 H87075	probable conserved
19	41	42.3	359	2 C83039	probable permealase
20	41	42.3	570	2 JC5722	vacuolar protein s
21	41	42.3	619	2 H84416	hypothetical prote
22	41	42.3	643	1 SL5623	El protein - human
23	41	42.3	713	2 JE0230	NADPH-cytochrome P
24	41	42.3	859	2 AE2217	hypothetical prote
25	41	42.3	909	2 T06246	aspartate kinase (
26	41	42.3	916	2 T06242	aspartate kinase (
27	41	42.3	1032	2 S74487	hypothetical prote
28	41	42.3	1055	2 C82600	multidrug-efflux t
29	40.5	41.8	795	2 B83608	hypothetical prote

30	40	41.2	101	2	G69203	conserved hypothet
31	40	41.2	109	2	F89886	hypothetical prote
32	40	41.2	137	2	A83751	hypothetical prote
33	40	41.2	179	2	D90167	conserved hypothet
34	40	41.2	189	2	S49846	asparagine synthas
35	40	41.2	217	1	GMPT4	gene 59 protein -
36	40	41.2	227	2	C75582	conserved hypothet
37	40	41.2	240	2	C89967	serine proteinase
38	40	41.2	302	2	T03109	probable membrane
39	40	41.2	327	2	S40753	hypothetical prote
40	40	41.2	357	1	A48511	protein-glutamate
41	40	41.2	374	2	G81926	probable polyamine
42	40	41.2	419	2	C81179	spermidine/putresc
43	40	41.2	454	2	AH2821	conserved hypothet
44	40	41.2	470	2	H97599	BH0982 hypothetica
45	40	41.2	584	2	T12989	asparagine synthas

ALIGNMENTS

RESULT 1

T16880  
hypothetical protein T14G12.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 05-Oct-2004  
C;Accession: T16880

R;Wilcox, L.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid T14G12.

A;Reference number: Z18596

A;Accession: T16880

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-270 <WT>

A;Cross-references: UNIPROT:Q22510; UNIPARC:UPI0000075025; EMBL:U41268; NID:g1086843; P1

C;Genetics:

A;Gene: CESP:T14G12.4

A;Introns: 37/1; 72/3; 164/1

F;93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;  
Best Local Similarity 57.1%; Pred. No. 2;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYTAPG 16

Db 205 GAAANLFPYFSPG 218

RESULT 2

JW0071

asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - soybean

C;Species: Glycine max (soybean)

C;Date: 13-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004

C;Accession: JW0071

R;Yamagata, H.; Nakajima, A.; Bowler, C.; Iwasaki, T.

Biosci. Biotechnol. Biochem. 62, 148-150, 1998

A;Title: Molecular cloning and characterization of a cDNA encoding asparagine synthetase

A;Reference number: JW0071; MUID:98162148; PMID:9501527

A;Accession: JW0071

A;Molecule type: mRNA

A;Residues: 1-579 <YAM>

A;Cross-references: UNIPROT:Q42792; UNIPARC:UPI00000A95EC; GB:U55874; NID:g1305548; PIDN

C;Superfamily: asparagine synthase (glutamine-hydrolysing)

C;Keywords: asparagine biosynthesis; ligase

F;2-579/Product: asparagine synthase (glutamine-hydrolysing) #status predicted <DUM>

F;2/Active site: Cys #status predicted

Query Match 47.4%; Score 46; DB 2; Length 579;

Best Local Similarity 34.4%; Pred. No. 10;

Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

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Qy 1 VDQK-----ATNIPPYTAGTK 18
    :|||  |||  |||  |||  |||
Db 462 IDGLKAHAEKHVTRDMLNANIPFPNTPTTK 493

RESULT 3
S69183
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - Lotus japonicus
C:Species: Lotus japonicus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S69183; S57932
R:Waterhouse, R.N.; Smyth, A.J.; Massonneau, A.; Prosser, I.M.; Clarkson, D.T.
Plant Mol. Biol. 30, 883-897, 1996
A>Title: Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus
A:Reference number: S69182; MUID:96270368; PMID:8639748
A:Accession: S69183
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-586 <WAT>
A:Cross-references: UNIPROT:P49093; UNIPARC:UPI000016DE2B; EMBL:X89410; NID:g897772; PID:
A:Experimental source: strain B-129
C:Genetics:
A:Gene: AS2
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)
C:Keywords: asparagine biosynthesis; ligase
F:2-586/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <DUM>
F:2/Active site: Cys #status predicted

Query Match 47.4%; Score 46; DB 2; Length 586;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

Qy 1 VDQK-----ATNIPPYTAGTK 18
    :|||  |||  |||  |||  |||
Db 462 IDGLKHAHAEKHVTRDMLNANIPFPNTPTTK 493

RESULT 4
AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Fitball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: UNIPROT:Q8ZHJ0; UNIPARC:UPI00000CD765; GB:AL590842; PIDN:CAC89747.1;
C:Genetics:
A:Gene: YPO0902

Query Match 47.4%; Score 46; DB 2; Length 658;
Best Local Similarity 52.9%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQKATNIPFYTAGT 17
    :|||  |||  |||  |||  |||
Db 99 LNGQKATNLAPATISST 115

RESULT 5
G59009
sensor histidine kinase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95009
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

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on, J.D.; Umavam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, J.;
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95009
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <KUR>
A:Cross-references: UNIPROT:Q9S1J1; UNIPARC:UPI0000051BF0; GB:AE005672;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0084

Query Match 46.4%; Score 45; DB 2; Length 350;
Best Local Similarity 72.7%; Pred. No. 8.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 NIPPYTAGTK 18
    |||  |||  |||  |||  |||
Db 248 NAFKYSAPGTK 258

RESULT 6
E97881
histidine kinase (EC 2.7.3.-) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E97881
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, F.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E97881
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <KUR>
A:Cross-references: UNIPROT:Q9S1J1; UNIPARC:UPI0000051BF0; GB:AE007317;
C:Genetics:
A:Gene: hk08
C:Keywords: phosphotransferase

Query Match 46.4%; Score 45; DB 2; Length 350;
Best Local Similarity 72.7%; Pred. No. 8.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 NIPPYTAGTK 18
    |||  |||  |||  |||  |||
Db 248 NAFKYSAPGTK 258

RESULT 7
AJPMW2
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - garden pea
N:Alternate names: asparagine synthetase (glutamine-hydrolyzing)
C:Species: Pisum sativum (garden pea)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S11443
R:Tsay, F.Y.; Coruzzi, G.M.
EMBO J. 9, 323-332, 1990
A>Title: Dark-induced and organ-specific expression of two asparagine synthetase genes i
A:Reference number: S11443; MUID:90151604; PMID:1968003
A:Accession: S11443
A:Molecule type: DNA
A:Residues: 1-583 <TSA>
A:Cross-references: UNIPROT:P19252; UNIPARC:UPI000016DF0B; EMBL:X52180; NID:g20651; PIDN:
C:Genetics:
A:Gene: AS2
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)

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C;Keywords: asparagine biosynthesis; ligase  
 F;2-583/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>  
 F;2/Active site: Cys #status predicted

Query Match 46.4%; Score 45; DB 1; Length 583;  
 Best Local Similarity 34.4%; Pred. No. 15;  
 Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQK-----ATNIFPYTAPGK 18  
 :|||:||||:||||:  
 Db 462 IDGLKAHAAKHVTDKMLNAGIPIPHNTNTK 493

RESULT 8  
 T16279  
 hypothetical protein F35H10.7 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: T16279  
 R;Woessner, J.  
 A;Submitted to the EMBL Data Library, November 1995  
 A;Description: The sequence of C. elegans cosmid F35H10.  
 A;Reference number: Z18490  
 A;Accession: T16279  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-511 <WDE>  
 A;Cross-references: UNIPROT:Q20069; UNIPARC:UPI000013790D; EMBL:U40934; NID:gi1072149; PI  
 C;Genetics:  
 A;Gene: CESP.F35H10.7  
 A;Introns: 15/2; 42/1; 67/2; 213/3; 252/2; 336/2; 484/3  
 C;Superfamily: Caenorhabditis elegans hypothetical protein F35H10.7

Query Match 45.4%; Score 44; DB 2; Length 511;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYTAPGK 18  
 :|||:||||:||||:  
 Db 26 GEKIVSVPHRKPKTK 41

RESULT 9  
 AD3488  
 transporter BMEI1890 [imported] - Brucella melitensis (strain 16M)  
 C;Species: Brucella melitensis  
 C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C;Accession: AD3488  
 R;DelVecchio, V.G.; Kaprat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
 ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A;Reference number: AD3252; PMID:11756688  
 A;Accession: AD3488  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-322 <KUR>  
 A;Cross-references: UNIPROT:Q8YE18; UNIPARC:UPI0000058245; GB:AE008917; PIDN:AAL53071.1;  
 A;Experimental source: strain 16M  
 C;Genetics:  
 A;Gene: BMEI1890  
 A;Map position: 1

Query Match 44.3%; Score 43; DB 2; Length 322;  
 Best Local Similarity 47.1%; Pred. No. 17;  
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DGKATNIFPYTAPGK 18  
 :|||:||||:||||:  
 Db 217 DGKADKLVSASAGVK 233

RESULT 10

AJPMN1  
 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [similarity] - garden pea  
 N;Alternate names: asparagine synthetase (glutamine-hydrolyzing)  
 C;Species: Pisum sativum (garden pea)  
 C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C;Accession: S11444  
 R;Tsai, F.Y.; Coruzzi, G.M.  
 EMBO J. 9, 323-332, 1990  
 A;Title: Dark-induced and organ-specific expression of two asparagine synthetase genes i  
 A;Reference number: S11443; MUID:90151604; PMID:1968003  
 A;Accession: S11444  
 A;Molecule type: DNA  
 A;Residues: 1-586 <TSA>  
 A;Cross-references: UNIPROT:P19251; UNIPARC:UPI000016DF0A; EMBL:X52179; NID:G20649; PIDN  
 C;Comment: This protein is one of a family of glutamine amidotransferases that have dual  
 : an aminator domain, which catalyzes the ammonia-dependent reaction, and a glutamine am  
 C;Genetics:  
 A;Gene: ASI  
 C;Superfamily: asparagine synthase (glutamine-hydrolyzing)  
 C;Keywords: asparagine biosynthesis; ligase  
 F;2-586/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>  
 F;175-586/Domain: aminator <AMN>  
 F;2/Active site: Cys #status predicted

Query Match 44.3%; Score 43; DB 1; Length 586;  
 Best Local Similarity 53.8%; Pred. No. 33;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATNIFPYTAPGK 18  
 :|||:||||:||||:  
 Db 482 ASHIFPNTNTK 494

RESULT 11  
 AF0306  
 putative trans-aconitate methyltransferase (EC 2.1.1.-) [imported] - Yersinia pestis (str  
 C;Species: Yersinia pestis  
 C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AF0306  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
 Nature 413, 523-527, 2001  
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: AF0306  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-258 <KUR>  
 A;Cross-references: UNIPROT:Q8ZDP7; UNIPARC:UPI00001368D0; GB:AL590842; PIDN:CAC91314.1;  
 C;Genetics:  
 A;Gene: tam  
 C;Superfamily: bioC protein; bioC homology  
 C;Keywords: methyltransferase

Query Match 43.3%; Score 42; DB 2; Length 258;  
 Best Local Similarity 50.0%; Pred. No. 20;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDQKATNIFPYTAPGK 18  
 :|||:||||:||||:  
 Db 200 VDMLRATGLRPLAPLPE 217

RESULT 12  
 AD2436  
 ATP-binding protein of polyamine ABC transporter all5044 [imported] - Nostoc sp. (strain  
 C;Species: Nostoc sp. PCC 7120  
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 31-Dec-2004  
 C;Accession: AD2436  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasaamoto, S.; Watanabe, A.; Iriguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AD2436  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-381 <KUR>  
A;Cross-references: UNIPROT:Q8YTM92; UNIPARC:UPI00000CED3F; GB:BA000019; PIDN:BAB76743.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all15044

Query Match 43.3%; Score 42; DB 2; Length 381;  
Best Local Similarity 53.3%; Pred. No. 31;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAP 15  
Db 80 IQGQPMWNIPIYRPP 94  
: ||| ||| ||| |||

RESULT 13  
AC2465  
6-phosphogluconate dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AC2465  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AC2465  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-476 <KUR>  
A;Cross-references: UNIPROT:Q8YTM3; UNIPARC:UPI00000CEB0D; GB:BA000019; PIDN:BAB76974.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr5275  
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

Query Match 43.3%; Score 42; DB 2; Length 476;  
Best Local Similarity 72.7%; Pred. No. 39;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 NIFPYTAPGTK 18  
Db 238 NIFPIDPETK 248  
||||| ||| |||

RESULT 14  
T22177  
hypochemical protein F44Fl.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22177  
R;Dobson, R.  
submitted to the EMBL Data Library, October 1996  
A;Reference number: Z19527  
A;Accession: T22177  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-623 <WIL>  
A;Cross-references: UNIPROT:O02260; UNIPARC:UPI000017B9C4; EMBL:Z81083; PIDN:CAB03101.1;  
A;Experimental source: clone F44F1  
C;Genetics:  
A;Gene: CESP:F44Fl.3  
A;Map position: 1  
A;Introns: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3

Query Match 43.3%; Score 42; DB 2; Length 623;

Best Local Similarity 50.0%; Pred. No. 53;  
Matches 11; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

Qy 1 VDGQKATNI-----PPYTAPGTK 18  
Db 152 VDGQWKTIIDDDYFPYTTDGIR 173  
||||| ||| ||| ||| |||

RESULT 15  
B71325  
conserved hypothetical protein TP0421 - syphilis spirochete  
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: B71325  
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A;Reference number: A71250; MUID:98332770; PMID:9665876  
A;Accession: B71325  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-683 <COL>  
A;Cross-references: UNIPROT:O83436; UNIPARC:UPI00000C0A71; GB:AE001220; GB:AE000520; NID  
A;Experimental source: strain Nichols  
C;Genetics:  
A;Gene: TP0421

Query Match 43.3%; Score 42; DB 2; Length 683;  
Best Local Similarity 50.0%; Pred. No. 59;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYTAPG 16  
Db 278 GQKSARFFGFSAPG 291  
||||| ||| ||| |||

Search completed: August 30, 2006, 04:30:53  
Job time : 12.7273 secs



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 70.1818 Seconds  
(without alignments)  
237.245 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDQKATNIPFYTPAGTK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	54.6	1143	2	Q3N7V1_9PROT
2	51	52.6	382	2	Q7P5V1_FUSNV
3	51	52.6	382	2	Q8R6B3_FUSNN
4	48	49.5	168	2	Q95QA9_CAEEL
5	48	49.5	270	2	Q22510_CAEEL
6	47	48.5	365	2	Q36VP1_RHOPA
7	47	48.5	1054	2	Q608X6_METCA
8	47	48.5	1538	2	Q94H26_ORYSA
9	46	47.4	497	2	Q9FYU1_CHLRE
10	46	47.4	579	2	P93168_SOYEN
11	46	47.4	579	2	Q38IA6_SOYEN
12	46	47.4	579	2	Q42792_SOYEN
13	46	47.4	579	2	Q9SM55_PHAVU
14	46	47.4	585	1	ASNS2_LOTJA
15	46	47.4	641	2	Q8CKM1_YERPE
16	46	47.4	658	2	Q8ZHU0_YERPE
17	45.5	46.9	491	2	Q212W7_BORAV
18	45	46.4	185	2	Q2TYB0_ASPOR
19	45	46.4	190	2	Q68E47_AERPU
20	45	46.4	279	2	Q619H6_CAEER
21	45	46.4	350	2	Q8DRK0_STRRG
22	45	46.4	350	2	Q9SLJ1_STRPN
23	45	46.4	445	1	ALN_STRCO
24	45	46.4	582	1	ASNS2_PEA
25	45	46.4	583	2	Q8RVL0_9FABA
26	44	45.4	131	1	SSB_STAES
27	44	45.4	131	2	Q5HMC5_STAEO
28	44	45.4	190	2	Q3VAY9_9SPHN
29	44	45.4	340	2	Q9AYA0_ORYSA
30	44	45.4	395	2	Q9ZHQ4_STRFR
31	44	45.4	476	2	Q3MA44_ANAVT

32 44 45.4 511 1 U171\_CAEEL  
33 44 45.4 525 2 Q6ALL1\_DESPS  
34 44 45.4 584 2 Q9MB61\_ASTSI  
35 44 45.4 586 2 Q84X69\_SECURIGERA  
36 44 45.4 589 2 Q53Q04\_ORYSA  
37 44 45.4 703 2 Q46LV7\_PROWT  
38 44 45.4 760 2 Q6UUM4\_ORYSA  
39 44 45.4 875 2 Q7FAL9\_ORYSA  
40 44 45.4 884 2 Q53JX1\_ORYSA  
41 44 45.4 908 2 Q2ZHO1\_CALSA  
42 44 45.4 1436 2 Q7FAL2\_ORYSA  
43 44 45.4 1685 2 Q7XSP1\_ORYSA  
44 44 45.4 1829 2 Q70XV6\_AMBTC  
45 44 45.4 2096 2 Q2R0G5\_ORYSA

#### ALIGNMENTS

RESULT 1  
Q3N7V1\_9PROT  
ID Q3N7V1\_9PROT PRELIMINARY; PRT; 1143 AA.  
AC Q3N7V1;  
DT 25-OCT-2005, integrated into UniprotKB/TREMBL.  
DT 25-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Putative type 4 fibrillar biogenesis protein PiliY precursor.  
GN ORFNames=NeutDRAFT\_0559;  
OS Nitrosomonas eutropha C71.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
OC Nitrosomonadaceae; Nitrosomonas.  
OX NCBI\_TaxID=335283;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C71;  
RG US DOE Joint Genome Institute (JGI-PGF);  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
RA Hammon N., Israni S., Pitluck S., Richardson P.;  
RT "Sequencing of the draft genome and assembly of Nitrosomonas eutropha C71."  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C71;  
RG US DOE Joint Genome Institute (JGI-ORNL);  
RA Larimer F., Land M., Hauser L.;  
RT "Annotation of the draft genome assembly of Nitrosomonas eutropha C71."  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
CC -|- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC  
DR EMBL; AJ01000019; EAC16686.1; -; Genomic\_DNA.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 1143 AA; 123766 MW; 9C270A88F6A0FAF1 CRC64;  
Query Match 54.6%; Score 53; DB 2; Length 1143;  
Best Local Similarity 62.5%; Pred. No. 16;  
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 DGQKATNIPFYTPAGT 17  
Db 383 DGSKLTHFFNTSPAT 398  
RESULT 2  
Q7P5V1\_FUSNV  
ID Q7P5V1\_FUSNV PRELIMINARY; PRT; 382 AA.

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AC Q7P5VL;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (BC 4.2.1.1-).
GN Name=FNW1343;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49256;
RA Kapatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyrpides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAF01000055; EAA24105.1; -; Genomic_DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
KW Lyase.
SQ SEQUENCE 382 AA; 43893 MW; 441C73816E1C761E CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGOKATNIFPYTAP 15
Db :||| |||||
28 EGKAVGIFPYAP 41

RESULT 3
Q8R6B3_FUSNN PRELIMINARY; PRT; 382 AA.
AC Q8R6B3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.1-).
GN OrderedLocustNames=FN0208;
OS Fusobacterium nucleatum subsp. nucleatum.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyrpides N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
CC -----
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CC -----
DR EMBL; AE009951; AAL94414.1; -; Genomic_DNA.
DR BiOCYC; FNUI90304:FN0208-MONOMER; -.
DR GO; GO:0016829; F:lyase activity; IEA.

DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
KW Lyase.
SQ SEQUENCE 382 AA; 43893 MW; 441C73816E1C761E CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGOKATNIFPYTAP 15
Db :||| |||||
28 EGKAVGIFPYAP 41

RESULT 4
Q95QA9_CAEEL PRELIMINARY; PRT; 168 AA.
AC Q95QA9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Forkhead transcription factor family protein 2, isoform b.
GN Name=fkh-2; ORFNames=TL4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
CC -----
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CC -----
DR EMBL; U41268; AAL02521.1; -; Genomic_DNA.
DR HSP; Q99958; IDSV.
DR SMR; Q95QA9; 2-68.
DR Ensembl; TL4G12.4; Caenorhabditis elegans.
DR WormBase; WSGene00001434; fkh-2.
DR WormPepe; TL4G12.4b; CE29342.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4E69968572 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKATNIFPYTAPG 16
Db :||| |||||
103 GAARANLFPPYSPG 116

RESULT 5
Q22510_CAEEL PRELIMINARY; PRT; 270 AA.
ID Q22510_CAEEL
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AC Q22510;  
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-FEB-2006, entry version 39.  
 DE Forkhead transcription factor family protein 2, isoform a.  
 GN Name=fkh-2; ORFNames=TI4G12.4;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;  
 RG The C. elegans sequencing consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 CC -1- INTERACTION:  
 CC Q2XW88.phd-3; NbExp=1; IntAct=EBI-327741, EBI-316766;  
 CC Q21648.R02F2.5; NbExp=1; IntAct=EBI-327741, EBI-314179;  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
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 CC EMBL; U41268; AAA82436.1; -; Genomic\_DNA.  
 DR PIR; T16880.  
 DR HSSP; Q99958; I05V.  
 DR SMR; Q22510; 93-170.  
 DR IntAct; Q22510; -.  
 DR Ensembl; T14G12.4; Caenorhabditis elegans.  
 DR WormBase; WBGene00001434; fkh-2.  
 DR WormPep; T14G12.4a; CE04965.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR InterPro; IPR001766; TF Fork head.  
 DR InterPro; IPR011991; Wing\_hlx\_DNA\_bd.  
 DR Pfam; PF00250; Fork head; 1.  
 DR PRINTS; PR00053; FORKHEAD.  
 DR ProDom; PD000425; TF Fork head; 1.  
 DR SMART; SM00339; FH; 1.  
 DR PROSITE; PS00657; FORK HEAD 1; 1.  
 DR PROSITE; PS00658; FORK HEAD 2; 1.  
 DR PROSITE; PS00039; FORK HEAD 3; 1.  
 KW Complete proteome; DNA-binding; Nuclear protein; Transcription;  
 KW Transcription regulation.  
 SQ SEQUENCE 270 AA; 30491 MW; 7C49116B5EC76175 CRC64;  
 Query Match 49.5%; Score 48; DB 2; Length 270;  
 Best Local Similarity 57.1%; Pred. No. 24;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 GQKATNIFPYTPAG 16  
 DB 205 GAAANLFFPYSPG 218  
 RESULT 6  
 ID Q36VF1\_RHOPA  
 AC Q36VF1;  
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.  
 DT 06-DEC-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Hypothetical protein.  
 GN ORFNames=RPEDRAFT\_0215;  
 OS Rhodopsudomonas palustris BisA53.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Rhodopsudomonas.  
 OX NCBI\_TaxID=316055;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BisA53;  
 Query Match 49.5%; Score 48; DB 2; Length 270;  
 Best Local Similarity 57.1%; Pred. No. 24;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 GQKATNIFPYTPAG 16  
 DB 205 GAAANLFFPYSPG 218  
 RESULT 6  
 ID Q36VF1\_RHOPA  
 AC Q36VF1;  
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.  
 DT 06-DEC-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Hypothetical protein.  
 GN ORFNames=RPEDRAFT\_0215;  
 OS Rhodopsudomonas palustris BisA53.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Rhodopsudomonas.  
 OX NCBI\_TaxID=316055;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BisA53;

RG US DOE Joint Genome Institute (JGI-RGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
 RA Hamon N., Israni S., Pitluck S., Richardson P.;  
 RT "Sequencing of the draft genome and assembly of Rhodopsudomonas  
 RT palustris BisA53."  
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BisA53;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome of Rhodopsudomonas palustris  
 RT BisA53."  
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC EMBL; AALA01000029; EAO87857.1; -; Genomic\_DNA.  
 DR EMBL; AALA01000029; EAO87857.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 365 AA; 40239 MW; E11D3C9BC0F1244F CRC64;  
 Query Match 48.5%; Score 47; DB 2; Length 365;  
 Best Local Similarity 50.0%; Pred. No. 48;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 VDGQKATNIFPYTPAG 16  
 DB 75 LDGLKAGQVPIYLPFG 90  
 RESULT 7  
 ID Q608X6\_METCA  
 AC Q608X6;  
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.  
 DT 23-NOV-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 9.  
 DE Hydrophobe/amphiphile Efflux-1 (HAEL) family protein.  
 GN OrderedLocustNames=MCA1360;  
 OS Methylococcus capsulatus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;  
 OC Methylococcaceae; Methylococcus.  
 OX NCBI\_TaxID=414;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bath / NCIMB 11132;  
 RX PubMed=15383840; DOI=10.1371/journal.pbio.0020303;  
 RA Ward N.L., Larsen O., Sakwa J., Bruseth L., Khouri H.M., Durkin A.S.,  
 RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,  
 RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,  
 RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,  
 RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,  
 RA Grindhaug S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S.,  
 RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,  
 RA Eisen J.A.;  
 RT "Genomic insights into methanotrophy: the complete genome sequence of  
 RT Methylococcus capsulatus (Bath).";  
 RL PLoS Biol. 2:1616-1628(2004).  
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 CC EMBL; AE017282; AAU92574.1; -; Genomic\_DNA.  
 DR TIGR; MCA1360; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001036; AcrIivn\_res.  
 DR InterPro; IPR004764; HAE1.



P93168 SOYBN PRELIMINARY; PRT; 579 AA.  
AC P93168;  
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-1997, sequence version 1.  
DT 07-FEB-2006, entry version 26.  
DE Asparagine synthetase 1 (EC 6.3.5.4).  
GN Name=AS1;  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
OC Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Century;  
RX MEDLINE=97188563; PubMed=9037148; DOI=10.1023/A:1005784202450;  
RA Hughes C.A., Beard H.S., Matthews B.F.;  
RT "Molecular cloning and expression of two cDNAs encoding asparagine  
RT synthetase in soybean.";  
RL Plant Mol. Biol. 33:301-311(1997).  
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CC  
CC  
DR EMBL; U77679; AAC49614.1; -; mRNA.  
DR HSSP; P22106; ICT9.  
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR006426; Asn\_synth\_AEB.  
DR InterPro; IPR001962; Asn\_synthase.  
DR InterPro; IPR00583; GATase\_2.  
DR Pfam; PF00733; Asn\_synthase; 1.  
DR Pfam; PF00310; GATase\_2; 1.  
DR TIGRFAMs; TIGR01536; asn\_synth\_AEB; 1.  
DR PROSITE; PS00443; GATASE\_TYPE\_II; UNKNOWN\_1.  
KW Ligase.  
SQ SEQUENCE 579 AA; 65366 MW; F7E80DA2019B0FC5 CRC64;  
Query Match 47.4%; Score 46; DB 2; Length 579;  
Best Local Similarity 34.4%; Pred. No. 1.2e+02;  
Matches 1; Conservative 2; Mismatches 5; Indels 14; Gaps 1;  
Qy 1 VDQK-----ATNIPPYTPAGTK 18  
Db 462 IDGLKAHAEKHVTDRLMLNANIPFPNTPTTK 493  
RESULT 11  
ID Q381A6 SOYBN PRELIMINARY; PRT; 579 AA.  
AC Q381A6;  
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.  
DT 22-NOV-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Asparagine synthetase.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
OC Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Lin S., Xiang W., Fan Z.;  
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.  
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CC  
CC  
DR EMBL; DQ227307; ABB04097.1; -; mRNA.

DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.  
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
SQ SEQUENCE 579 AA; 65219 MW; 3F3A9F62EA447A17 CRC64;  
Query Match 47.4%; Score 46; DB 2; Length 579;  
Best Local Similarity 34.4%; Pred. No. 1.2e+02;  
Matches 1; Conservative 2; Mismatches 5; Indels 14; Gaps 1;  
Qy 1 VDQK-----ATNIPPYTPAGTK 18  
Db 462 IDGLKAHAEKHVTDRLMLNANIPFPNTPTTK 493  
RESULT 12  
ID Q42792 SOYBN PRELIMINARY; PRT; 579 AA.  
AC Q42792;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE Asparagine synthetase (EC 6.3.5.4).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
OC Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Corsoy;  
RX MEDLINE=98162148; PubMed=95015127;  
RA Yamagata H., Nakajima A., Bowler C., Iwasaki T.;  
RT "Molecular cloning and characterization of a cDNA encoding asparagine  
RT synthetase from soybean (Glycine max L.) cell cultures";  
RL Biosci. Biotechnol. Biochem. 62:148-150(1998).  
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CC  
CC  
DR EMBL; U55874; AAC09952.1; -; mRNA.  
DR PIR; JMW0071; JMW0071.  
DR HSSP; P22106; ICT9.  
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR006426; Asn\_synth\_AEB.  
DR InterPro; IPR001962; Asn\_synthase.  
DR InterPro; IPR00583; GATase\_2.  
DR Pfam; PF00733; Asn\_synthase; 1.  
DR Pfam; PF00310; GATase\_2; 1.  
DR TIGRFAMs; TIGR01536; asn\_synth\_AEB; 1.  
DR PROSITE; PS00443; GATASE\_TYPE\_II; UNKNOWN\_1.  
KW Ligase.  
SQ SEQUENCE 579 AA; 65231 MW; B6E7B7902DF2BC95 CRC64;  
Query Match 47.4%; Score 46; DB 2; Length 579;  
Best Local Similarity 34.4%; Pred. No. 1.2e+02;  
Matches 1; Conservative 2; Mismatches 5; Indels 14; Gaps 1;  
Qy 1 VDQK-----ATNIPPYTPAGTK 18  
Db 462 IDGLKAHAEKHVTDRLMLNANIPFPNTPTTK 493  
RESULT 13  
ID Q9SM55 PHAVU PRELIMINARY; PRT; 579 AA.  
AC Q9SM55;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 21.

DE Asparagine synthetase (Type-I) (EC 6.3.5.4).

GN Name=asi;

QS Phaseolus vulgaris (Kidney bean) (French bean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

OC Phaseolus.

OC NCBI\_TaxID=3885;

RL NCB1\_TaxID=3885;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Great Northern; TISSUE=Root;

RA Galvez-Valdivieso G., Osuna D., Perez-Vicente R., Pineda M.,

RA Aguilar M.;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL; AJ13522; CAB57292.1; -; mRNA.

DR HSPB; P22106; 1CT9.

DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . ; IEA.

DR GO; GO:0016874; F:ligase activity; IEA.

DR GO; GO:0006529; P:asparagine biosynthesis; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR DR InterPro; IPR006426; Asn\_synth\_AEB.

DR DR InterPro; IPR001962; Asn\_synthase.

DR DR InterPro; IPR000583; GATase\_2.

DR DR Pfam; PF00733; Asn\_synthase; 1.

DR DR Pfam; PF00310; GATase\_2; 1.

DR DR TIGRFAMS; TIGR01536; asn\_synth\_AEB; 1.

DR DR PROSITE; PS00443; GATASE\_TYPE\_II; UNKNOWN\_1.

KW Ligase.

QY SEQUENCE 579 AA; 65266 MW; 7A74F5AE852CE2E6 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;

Best Local Similarity 34.4%; Pred. No. 1.2e+02;

Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps

Qy 1 VDGQK-----ATNIFPYTACGK 18

Db 462 IDGLKGAEKHVTRDMMNAANIFFPNTPTK 493

RESULT 14

ASNS2\_LOTJA

ID ASNS2\_LOTJA STANDARD; PRT; 595 AA.

AC P49093;

DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.

DT 01-FEB-1996, sequence version 1.

DT 07-FEB-2006, entry version 39.

DE Asparagine synthetase [glutamine-hydrolyzing] 2 (EC 6.3.5.4)

DE (Glutamine-dependent asparagine synthetase 2).

DE Name=AS2;

OS Lotus japonicus.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.

OC NCB1\_TaxID=34305;

RL NUCLEOTIDE SEQUENCE [MRNA].

RP STRAIN=cv. Gifu / B-129;

EX MEDLINE=96270368; PubMed=8639748;

RA Waterhouse R.N., Smyth A.J., Masson A., Prosser I.M.,

RA Clarkson D.T.;

RT "Molecular cloning and characterisation of asparagine synthetase from

RT Lotus japonicus: dynamics of asparagine synthesis in N-sufficient

RT conditions".

RL Plant Mol. Biol. 30:883-897(1996).

CC -!- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP +

CC diphosphate + L-asparagine + L-glutamate.

CC -!- PATHWAY: Asparagine biosynthesis.

CC -!- SIMILARITY: Contains 1 asparagine synthetase domain.

CC -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.

KW Hypothetical protein.

SQ SEQUENCE 641 AA; 62094 MW; A595153FEE45162 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 641;

Best Local Similarity 52.9%; Pred. No. 1.3e+02;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAPGT 17

Db 82 LMGQKATNLPATISST 98

Search completed: August 30, 2006, 04:29:13

Job time : 74.1818 secs

**This Page Blank (uspto)**



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 17.8182 Seconds  
(without alignments)  
88.424 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97

Sequence: 1 VDCQKATNIPYPATGK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	108	2	US-09-281-760E-35
2	97	100.0	312	2	US-09-701-623C-2
3	97	100.0	426	1	US-08-336-583-2
4	97	100.0	426	5	PCT-US95-13795-2
5	87	89.7	431	2	US-09-479-614-14
6	87	89.7	496	2	US-09-479-614-2
7	87	89.7	496	2	US-09-479-614-29
8	73	75.3	343	2	US-09-401-636-7
9	58	59.8	341	2	US-09-401-636-3
10	58	59.8	341	2	US-09-401-636-4
11	58	59.8	341	2	US-09-401-636-6
12	58	59.8	341	2	US-09-401-636-9
13	58	59.8	341	2	US-09-401-636-11
14	58	59.8	342	2	US-09-401-636-5
15	58	59.8	342	2	US-09-401-636-8
16	58	59.8	345	2	US-09-401-636-10
17	46	47.4	135	2	US-09-252-991A-30004
18	46	47.4	497	2	US-10-077-699C-5
19	45	46.4	350	2	US-09-094-103-6
20	45	46.4	350	2	US-09-080-963-2
21	45	46.4	350	2	US-08-947-251-2
22	45	46.4	350	2	US-09-769-787-89
23	45	46.4	358	2	US-09-583-110-5009
24	45	46.4	358	2	US-09-107-433-2960
25	45	46.4	583	7	US-09-252-991A-30004
26	44	45.4	121	2	US-09-710-279-2524

Patent No. 5256558  
Sequence 2524, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-281-760E-35  
; Sequence 35, Application US/09281760E  
; Patent No. 6734287  
; GENERAL INFORMATION:

APPLICANT: Lawton, Robert  
APPLICANT: Mermer, Brion  
TITLE OF INVENTION: Specific Binding Protein for Treating  
TITLE OF INVENTION: Canine Allergy  
FILE REFERENCE: 01-1275A  
CURRENT APPLICATION NUMBER: US/09/281,760E  
CURRENT FILING DATE: 1999-03-30  
PRIOR APPLICATION NUMBER: 09/058,331  
PRIOR FILING DATE: 1998-04-09  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 35  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Canis familiaris  
NAME/KEY: misc feature  
LOCATION: (81)..(81)  
OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,  
OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (82)..(82)  
OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (136)..(136)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (413)..(414)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (451)..(451)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (460)..(462)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (500)..(500)

Sequence 4212, Ap  
Sequence 10, Appl  
Patent No. 5256558  
Sequence 12884, A  
Sequence 6, Appl  
Sequence 66, Appl  
Sequence 6, Appl  
Sequence 66, Appl  
Sequence 6, Appl  
Sequence 8106, Ap  
Sequence 66, Appl  
Sequence 1, Appl  
Sequence 7, Appl  
Sequence 1, Appl  
Sequence 26880, A  
Sequence 4924, Ap  
Sequence 27624, A  
Sequence 29, Appl

27 44 45.4 132 2 US-09-134-001C-4212  
28 43 44.3 476 2 US-08-840-767-10  
29 43 44.3 585 7 5256558-2  
30 42 43.3 557 2 US-09-902-540-12884  
31 42 43.3 985 2 US-09-993-777-66  
32 42 43.3 985 2 US-09-993-777-66  
33 42 43.3 985 2 US-09-994-064-6  
34 42 43.3 985 2 US-09-994-064-66  
35 42 43.3 985 5 PCT-US96-03916-6  
36 42 43.3 985 5 PCT-US96-03916-66  
37 41 42.3 232 2 US-09-489-039A-8106  
38 41 42.3 570 1 US-08-967-364-1  
39 41 42.3 570 1 US-08-967-364-7  
40 41 42.3 570 2 US-09-368-408-1  
41 41 42.3 570 2 US-09-368-408-7  
42 41 42.3 1364 2 US-09-252-991A-26880  
43 40.5 41.8 464 2 US-09-543-681A-4924  
44 40.5 41.8 608 2 US-09-252-991A-27624  
45 40 41.2 63 2 US-09-612-402B-29

OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (5307)..(530)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (568)..(568)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (847)..(849)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8537)..(853)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1382)..(1382)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1832)..(1832)  
OTHER INFORMATION: "n" stands for any nucleic acid  
US-09-281-760E-35

Query Match 100.0%; Score 97; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.6e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGK 18  
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Db 47 VDGQKATNIFPYTAPGK 64  
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## RESULT 2

US-09-701-623C-2  
Sequence 2, Application US/09701623C  
Patent No. 6811782  
GENERAL INFORMATION:  
APPLICANT: Wang Ph.D., Chang Yi  
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY  
FILE REFERENCE: 11514153US1  
CURRENT APPLICATION NUMBER: US/09/701,623C  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US99/13959  
PRIOR FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: 09/100,287  
PRIOR FILING DATE: 1998-06-20  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2

LENGTH: 312

TYPE: PRT

ORGANISM: Dog

FEATURE:

OTHER INFORMATION: CH2CH3n of dog IgE

PUBLICATION INFORMATION:

AUTHORS: Patel,

JOURNAL: Immunogenetics

VOLUME: 41

PAGES: 282-286

DATE: 1995

US-09-701-623C-2

Query Match 100.0%; Score 97; DB 2; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGK 18  
|||||

Db 48 VDGQKATNIFPYTAPGK 65

## RESULT 3

US-08-336-583-2  
Sequence 2, Application US/08336583  
Patent No. 5629415  
GENERAL INFORMATION:  
APPLICANT: HOLLIS, GREGORY F.  
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHRISTINE E. CARTY  
STREET: 126 E. LINCOLN AVENUE  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,583  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: CARTY, CHRISTINE E.  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 19211  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4720  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-583-2

Query Match 100.0%; Score 97; DB 1; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGK 18  
|||||

Db 146 VDGQKATNIFPYTAPGK 163  
|||||

## RESULT 4

PCT-US95-13795-2  
Sequence 2, Application PC/TUS9513795  
GENERAL INFORMATION:  
APPLICANT: HOLLIS, GREGORY F.  
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHRISTINE E. CARTY  
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match 100.0%; Score 97; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPPYTAPGTK 18
Db 146 VDGQKATNIPPYTAPGTK 163

RESULT 5
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 89.7%; Score 87; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPPYTAPG 16
Db 151 VDGQKATNIPPYTAPG 166

RESULT 6
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34

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; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6
Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYP 13
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Db      62 VDGQKATNIPFYP 74
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RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9
Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYP 13
||||| |:|||||
Db      62 VDGQKATNIPFYP 74
||||| |:|||||

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
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; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPPYT 13
Db      62 VDGQEAENLFPYT 74
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RESULT 14
US-09-401-636-5
; Sequence 5, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-5

Query Match      59.8%; Score 58; DB 2; Length 342;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPPYT 13
Db      62 VDGQEAENLFPYT 74
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RESULT 15
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match      59.8%; Score 58; DB 2; Length 342;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPPYT 13
Db      62 VDGQEAENLFPYT 74
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 90.9091 Seconds  
(without alignments)  
91.717 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97  
Sequence: 1 VDGQKATNIPFYTAGTK 18

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Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-9
2	97	100.0	312	5	US-10-723-207-2
3	97	100.0	426	4	US-10-214-524-28
4	87	89.7	18	5	US-10-758-165-10
5	87	89.7	431	3	US-09-479-614-14
6	87	89.7	431	4	US-10-409-772-14
7	87	89.7	496	3	US-09-479-614-2
8	87	89.7	496	3	US-09-479-614-29
9	87	89.7	496	4	US-10-214-524-25
10	87	89.7	496	4	US-10-409-772-2
11	87	89.7	496	4	US-10-409-772-29
12	73	75.3	343	3	US-09-401-636-7
13	73	75.3	343	4	US-10-176-664-7
14	73	75.3	343	4	US-10-673-594-7
15	73	75.3	577	4	US-10-214-524-29
16	58	59.8	337	4	US-10-438-794-3
17	58	59.8	337	4	US-10-453-915-3
18	58	59.8	338	4	US-10-438-794-6
19	58	59.8	338	4	US-10-453-915-6
20	58	59.8	341	3	US-09-401-636-3
21	58	59.8	341	3	US-09-401-636-4
22	58	59.8	341	3	US-09-401-636-6
23	58	59.8	341	3	US-09-401-636-9
24	58	59.8	341	3	US-09-401-636-11
25	58	59.8	341	4	US-10-176-664-3
26	58	59.8	341	4	US-10-176-664-4
27	58	59.8	341	4	US-10-176-664-6

28 58 59.8 341 4 US-10-176-664-9  
29 58 59.8 341 4 US-10-176-664-11  
30 58 59.8 341 4 US-10-673-594-3  
31 58 59.8 341 4 US-10-673-594-4  
32 58 59.8 341 4 US-10-673-594-6  
33 58 59.8 341 4 US-10-673-594-9  
34 58 59.8 341 4 US-10-673-594-11  
35 58 59.8 342 3 US-09-401-636-5  
36 58 59.8 342 3 US-09-401-636-8  
37 58 59.8 342 4 US-10-176-664-5  
38 58 59.8 342 4 US-10-176-664-8  
39 58 59.8 342 4 US-10-673-594-5  
40 58 59.8 342 4 US-10-673-594-8  
41 58 59.8 345 3 US-09-401-636-10  
42 58 59.8 345 4 US-10-176-664-10  
43 58 59.8 345 4 US-10-673-594-10  
44 58 59.8 347 4 US-10-438-794-14  
45 58 59.8 347 4 US-10-453-915-14

#### ALIGNMENTS

##### RESULT 1

US-10-758-165-9

; Sequence 9, Application US/10758165

; Publication No. US20050196816A1

; GENERAL INFORMATION:

; APPLICANT: Hammerberg, Bruce

; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

; FILE REFERENCE: 5051-661

; CURRENT APPLICATION NUMBER: US/10758,165

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: US 60/440,472

; PRIOR FILING DATE: 2003-01-16

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Canis familiaris

US-10-758-165-9

Query Match 100.0%; Score 97; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGTK 18

Db 1 VDGQKATNIPFYTAGTK 18

##### RESULT 2

US-10-723-207-2

; Sequence 2, Application US/10723207

; Publication No. US20050250934A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; APPLICANT: Walfield, Alan M.

; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

; FILE REFERENCE: 1151-4153US2

; CURRENT APPLICATION NUMBER: US/10723,207

; CURRENT FILING DATE: 2003-11-24

; PRIOR APPLICATION NUMBER: 09/701,623

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US99/13959

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 09/100,287

; PRIOR FILING DATE: 1998-06-20

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 2

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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match      100.0%; Score 97; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGKATNIPFYTAGTK 18
Db      48 VDGKATNIPFYTAGTK 65

RESULT 3
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Mia
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00103.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match      100.0%; Score 97; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGKATNIPFYTAGTK 18
Db      146 VDGKATNIPFYTAGTK 163

RESULT 4
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-861
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10
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Query Match      89.7%; Score 87; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGKATNIPFYTAGP 16
Db      1 VDGKATNIPFYTAGP 16

RESULT 5
US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14
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Query Match      89.7%; Score 87; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGKATNIPFYTAGP 16
Db      151 VDGKATNIPFYTAGP 166
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RESULT 6
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14
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Query Match      89.7%; Score 87; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGKATNIPFYTAGP 16
Db      151 VDGKATNIPFYTAGP 166
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RESULT 7
US-09-479-614-2
; Sequence 2, Application US/09479614
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; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
Query Match      89.7%; Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAGP 16
Db      216 VDGOKATNIPPYTAGP 231

RESULT 8
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29
Query Match      89.7%; Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAGP 16
Db      216 VDGOKATNIPPYTAGP 231

RESULT 9
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61

; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
Query Match      89.7%; Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAGP 16
Db      216 VDGOKATNIPPYTAGP 231

RESULT 10
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
Query Match      89.7%; Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAGP 16
Db      216 VDGOKATNIPPYTAGP 231

RESULT 11
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
Query Match      89.7%; Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAGP 16
Db      216 VDGOKATNIPPYTAGP 231
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Db      216 VDGQKATNIPFYTAP 231

RESULT 12
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-7

Query Match      75.3%; Score 73; DB 3; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAP 15
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Db      61 VDGQKAENLFFYTAP 75

RESULT 13
US-10-176-664-7
; Sequence 7, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAP 15
      ||||| :|||
Db      61 VDGQKAENLFFYTAP 75

RESULT 14
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0038;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAP 15
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Db      295 VDGQKAENLFFYTAP 309

Search completed: August 30, 2006, 05:13:00
Job time : 91.9091 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 9.27273 Seconds  
(without alignments)  
133.695 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97

Sequence: 1 VDGQKATNIPYTPGKTK 18

Scoring table: BLOSUM62

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Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.\*

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- 2: /EMC\_Celerra\_SID3S/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /EMC\_Celerra\_SID3S/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /EMC\_Celerra\_SID3S/ptodata/1/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 5: /EMC\_Celerra\_SID3S/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 6: /EMC\_Celerra\_SID3S/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /EMC\_Celerra\_SID3S/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /EMC\_Celerra\_SID3S/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	47.4	80	7	US-11-330-403-2450
2	46	47.4	239	7	US-11-330-403-3689
3	46	47.4	250	7	US-11-330-403-15600
4	46	47.4	287	7	US-11-330-403-17777
5	46	47.4	579	7	US-11-330-403-2402
6	46	47.4	579	7	US-11-330-403-6386
7	46	47.4	579	7	US-11-330-403-6386
8	46	47.4	579	7	US-11-330-403-18232
9	46	47.4	581	7	US-11-330-403-1293
10	46	47.4	586	7	US-11-330-403-4518
11	45.5	46.9	581	7	US-11-330-403-7358
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13	45	46.4	583	7	US-11-330-403-13229
14	45	46.4	583	7	US-11-330-403-14971
15	44	45.4	584	7	US-11-330-403-5521
16	44	45.4	586	7	US-11-330-403-482
17	43	44.3	254	6	US-10-471-571A-726
18	43	44.3	586	7	US-11-330-403-10108
19	43	44.3	586	7	US-11-330-403-14969
20	42.5	43.8	236	7	US-11-375-221-16
21	42	43.3	585	7	US-11-330-403-13141
22	42	43.3	644	7	US-11-330-403-6482
23	42	43.3	644	7	US-11-330-403-15095
24	42	43.3	985	7	US-11-342-171-6
25	42	43.3	985	7	US-11-342-171-66

26 41.5 42.8 582 7 US-11-330-403-14312 Sequence 14312, A  
27 41.5 42.8 582 7 US-11-330-403-15230 Sequence 15230, A  
28 41 42.3 570 6 US-10-511-937-2612 Sequence 2612, Ap  
29 40.5 41.8 582 7 US-11-330-403-15597 Sequence 15597, A  
30 40 41.2 189 7 US-11-330-403-12759 Sequence 12759, A  
31 40 41.2 332 7 US-11-056-3558-11318 Sequence 11318, A  
32 40 41.2 339 6 US-10-449-902-30393 Sequence 30393, A  
33 40 41.2 339 6 US-10-449-902-36927 Sequence 36927, A  
34 40 41.2 339 6 US-10-449-902-51715 Sequence 51715, A  
35 40 41.2 339 7 US-11-056-3558-11317 Sequence 11317, A  
36 40 41.2 377 7 US-11-056-3558-11316 Sequence 11316, A  
37 40 41.2 422 6 US-10-953-349-22933 Sequence 22933, A  
38 40 41.2 422 6 US-11-056-3558-54494 Sequence 54494, A  
39 40 41.2 451 6 US-10-953-349-49331 Sequence 49331, Ap  
40 41.2 451 7 US-11-056-3558-35016 Sequence 35016, A  
41 40 41.2 451 7 US-11-056-3558-101754 Sequence 101754, A  
42 40 41.2 451 7 US-11-056-3558-112993 Sequence 112993, A  
43 40 41.2 467 6 US-10-953-349-22932 Sequence 22932, A  
44 40 41.2 467 7 US-11-056-3558-54493 Sequence 54493, A  
45 40 41.2 469 6 US-10-953-349-49330 Sequence 49330, Ap

#### ALIGNMENTS

RESULT 1  
US-11-330-403-2450  
; Sequence 2450, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 2450  
; LENGTH: 80  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-330-403-2450

Query Match 47.4%; Score 46; DB 7; Length 80;  
Best Local Similarity 34.4%; Pred. No. 0.93;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDGOK-----ATNIPFPYTPGKTK 18  
|||  
Db 27 IDGLKAHAEKHVTRMMLNANIPFPNPTTK 58  
|||

RESULT 2  
US-11-330-403-3689  
; Sequence 3689, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 3689  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(239)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-11-330-403-3689

Query Match 47.4%; Score 46; DB 7; Length 239;

Best Local Similarity 34.4%; Pred. No. 3;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIFPYTAPGK 18  
: || |  
Db 131 IDGLKAHAEKHVTDRLMLNAAANIFFPNTPTTK 162

## RESULT 3

US-11-330-403-15600  
; Sequence 15600, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 15600  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-330-403-15600

Query Match 47.4%; Score 46; DB 7; Length 250;  
Best Local Similarity 34.4%; Pred. No. 3.2;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIFPYTAPGK 18  
: || |  
Db 131 IDGLKAHAEKHVTDRLMLNAAANIFFPNTPTTK 162

## RESULT 4

US-11-330-403-17777  
; Sequence 17777, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 17777  
; LENGTH: 287  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-330-403-17777

Query Match 47.4%; Score 46; DB 7; Length 287;  
Best Local Similarity 34.4%; Pred. No. 3.7;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIFPYTAPGK 18  
: || |  
Db 170 IDGLKAHAEKHVTDRLMLNAAANIFFPNTPTTK 201

## RESULT 5

US-11-330-403-2402  
; Sequence 2402, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 2402  
; LENGTH: 579

; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-330-403-2402

Query Match 47.4%; Score 46; DB 7; Length 579;  
Best Local Similarity 34.4%; Pred. No. 8;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIFPYTAPGK 18  
: || |  
Db 462 IDGLKAHAEKHVTDRLMLNAAANIFFPNTPTTK 493

## RESULT 6

US-11-330-403-6386  
; Sequence 6386, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 6386  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Phaseolus vulgaris  
US-11-330-403-6386

Query Match 47.4%; Score 46; DB 7; Length 579;  
Best Local Similarity 34.4%; Pred. No. 8;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIFPYTAPGK 18  
: || |  
Db 462 IDGLKAHAEKHVTDRLMLNAAANIFFPNTPTTK 493

## RESULT 7

US-11-330-403-11265  
; Sequence 11265, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 11265  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-330-403-11265

Query Match 47.4%; Score 46; DB 7; Length 579;  
Best Local Similarity 34.4%; Pred. No. 8;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIFPYTAPGK 18  
: || |  
Db 462 IDGLKAHAEKHVTDRLMLNAAANIFFPNTPTTK 493

## RESULT 8

US-11-330-403-18232  
; Sequence 18232, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B

```
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 18232
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-18232

Query Match      47.4%; Score 46; DB 7; Length 579;
Best Local Similarity 34.4%; Pred. No. 8;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy      1 VDGQK-----ATNIFPYTPGTK 18
      :|||
Db      462 IDGLKAHAEKHVTDRLMLNAANIFPNTPTTK 493

RESULT 9
US-11-330-403-1293
; Sequence 1293, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 1293
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(581)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-1293

Query Match      47.4%; Score 46; DB 7; Length 581;
Best Local Similarity 34.4%; Pred. No. 8;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy      1 VDGQK-----ATNIFPYTPGTK 18
      :|||
Db      463 IDGLKAHAEKHVTDRLMLNAANIFPNTPTTK 494

RESULT 10
US-11-330-403-4518
; Sequence 4518, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4518
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Lotus corniculatus var. japonicus
US-11-330-403-4518

Query Match      47.4%; Score 46; DB 7; Length 586;
Best Local Similarity 31.2%; Pred. No. 8.1;
Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

Qy      1 VDGQK-----ATNIFPYTPGTK 18
      :|||
Db      462 IDGLKAHAEKHVTDRLMLNAANIFPNTPTTK 493

; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 7358
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(581)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-7358

Query Match      46.9%; Score 45.5; DB 7; Length 581;
Best Local Similarity 33.3%; Pred. No. 9.7;
Matches 11; Conservative 2; Mismatches 5; Indels 15; Gaps 1;

Qy      1 VDGQK-----ATNIFPYTPGTK 18
      :|||
Db      462 IDGLKAHAEKHVTDRLMLNAANIFPNTPTTK 494

RESULT 11
US-11-330-403-7358
; Sequence 7358, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 7358
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(581)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-7358

Query Match      46.4%; Score 45; DB 7; Length 64;
Best Local Similarity 72.7%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      8 NIPFYTPGTK 18
      :|||
Db      10 NIMPYNFPGTK 20

RESULT 12
US-11-375-095-104
; Sequence 104, Application US/11375095
; Publication No. US20060156443A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: VAN, HUA
; APPLICANT: RICHARD, CRAIG
; APPLICANT: BRINKERHOFF, W. LEIGH
; APPLICANT: SWORDS, KATHY M. M.
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162
; CURRENT APPLICATION NUMBER: US/11/375,095
; CURRENT FILING DATE: 2006-03-15
; PRIOR APPLICATION NUMBER: US/10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-375-095-104

Query Match      46.4%; Score 45; DB 7; Length 64;
Best Local Similarity 72.7%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      8 NIPFYTPGTK 18
      :|||
Db      10 NIMPYNFPGTK 20

RESULT 13
US-11-330-403-13229
; Sequence 13229, Application US/11330403
```

```

; Publication No. US20060159563A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Abad, Mark S.
;
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
;
; FILE REFERENCE: 38-21(53629)B
;
; CURRENT APPLICATION NUMBER: US/11/330,403
;
; CURRENT FILING DATE: 2006-01-12
;
; NUMBER OF SEQ ID NOS: 19250
;
; SEQ ID NO 13229
;
; LENGTH: 583
;
; TYPE: PRT
;
; ORGANISM: Securigera parviflora
;
US-11-330-403-13229

```

Query Match	46.4%;	Score 45;	DB 7;	Length 583;
Best Local Similarity	34.4%;	Pred. No. 12;		
Matches 11: Conservative	2;	Mismatches 5;	Indels 14;	Gaps 1;

QY 1 VDGQK-----ATNIFPYTAPGTK 18  
:||| | ||||: |||  
Db 461 IDGLKEHAAKHVTDKIMFNAANIFPHNTPTTK 492

```

RESULT 14
US-11-330-403-14971
; Sequence 14971, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21 (53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 14971
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Pisum sativum
US-11-330-403-14971

```

Query Match	46.4%;	Score 45;	DB 7;	Length 583;
Best Local Similarity	34.4%;	Pred. No. 12;		
Matches 11: Conservative	2;	Mismatches 5;	Indels 14;	Gaps 1;

QY 1 VDGQK-----ATNIFPYTAPGK 18  
:||| | | | | : |||  
Dp 462 IDGLKAHAAKHVTDKMLNAGNIFPHNTPTNK 493

```

RESULT 15
US-11-330-403-5521
; Sequence 5521, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 5521
; LENGTH: 584
; TYPE: PRT
; ORGANISM: Astragalus sinicus
US-11-330-403-5521

```

Query Match	45.4%;	Score 44;	DB 7;	Length 584;
Best Local Similarity	46.7%;	Pred. No. 18;		
Matches	7;	Conservative.	3;	Mismatches 5; Indels 0; Gaps 0;

**Qy**            4 QKATNIFPYTAPGTK 18  
               : |||::||  
**Db**            479 RNAANIYPHNTPTSK 493

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 65.4545 Seconds  
(without alignments)  
125.735 Million cell updates/sec

Title: US-10-758-165a-10  
Perfect score: 97  
Sequence: 1 VDGQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq.8.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*  
10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	ADRL0610	Cat IgE e
2	97	100.0	431	ADG73237	Cat immun
3	97	100.0	496	ABP96580	Cat IgE h
4	97	100.0	496	ABU09338	Feline Ig
5	97	100.0	496	ABU09336	Feline Ig
6	97	100.0	496	ADG73251	Cat parti
7	97	100.0	496	ADG73225	Cat parti
8	87	89.7	18	ADRL0609	Dog IgE e
9	87	89.7	312	AAV79995	Dog immun
10	87	89.7	417	AAW23067	Canine Ig
11	87	89.7	426	AAW97753	Canine Ig
12	87	89.7	426	ABP96583	Dog IgE h
13	77	79.4	577	ABP96584	Duckbille
14	72	74.2	343	3 AAB06204	Platypus
15	60	61.9	337	ADG90022	Opossum-r
16	60	61.9	337	ADN00643	ORO prote
17	60	61.9	338	ADG90025	Opossum-h
18	60	61.9	338	ADN00646	OSO prote
19	60	61.9	341	3 AAB06206	Immunogen
20	60	61.9	341	3 AAB03644	Opossum I
21	60	61.9	341	3 AAB06208	Immunogen
22	60	61.9	342	3 AAB06205	Immunogen
23	60	61.9	345	3 AAB06207	Immunogen

24	60	61.9	347	8	ADF90033	Adf90033 Opossum-h
25	60	61.9	347	8	ADN00654	OSO-H pro
26	60	61.9	353	8	ADN00661	H-OCO-H p
27	60	61.9	427	6	ABP96591	Brushtail
28	60	61.9	446	6	ABP96587	Opossum I
29	60	61.9	555	8	ADG90027	Opossum-r
30	60	61.9	555	8	ADN00648	ORORO pro
31	60	61.9	557	8	ADF90031	Opossum-h
32	60	61.9	557	8	ADG90035	Opossum-h
33	60	61.9	557	8	ADN00656	OSO pro
34	60	61.9	557	8	ADN00652	modOSO
35	60	61.9	566	8	ADG90029	Opossum-h
36	60	61.9	566	8	ADG90037	Opossum-h
37	60	61.9	566	8	ADN00658	OSO-H p
38	60	61.9	566	8	ADN00650	modOSO-H
39	55	56.7	18	8	ADRL0612	Sheep Ige
40	55	56.7	341	3	AAB06202	Immunogen
41	55	56.7	342	3	AAB06201	Immunogen
42	55	56.7	567	6	ABP96588	Pig Ige h
43	44	45.4	87	3	AAV83167	PAGE1 pol
44	44	45.4	99	7	ADG42685	Human PAG
45	44	45.4	99	7	ADJ55754	Peptide h

## ALIGNMENTS

RESULT 1  
ADRL0610  
ID ADR10610 standard; peptide; 18 AA.  
XX  
AC ADR10610;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Cat IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.  
XX  
KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW cat.  
XX  
OS Felis catus.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PP 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
DR WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IgE epitope, useful  
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian IgE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
CC residues 357-371 (ADRL0601) and 146-162 (ADRL0609) respectively of the

CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC cat IgE 3.76 recognition site.  
 XX  
 XX Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGKQ 18  
 |||||  
 Db 1 VDGQKATNIFPYTAPGKQ 18

RESULT 2  
 ADG73237  
 ID ADG73237 standard; protein; 431 AA.

XX AC ADG73237;  
 XX DT 11-MAR-2004 (first entry)

XX Cat immunoglobulin E (IgE) constant region.

XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;  
 XX immune response; IgE-mediated response; allergy; cat; constant region.  
 XX Felis catus.

XX US2003216565-A1.

XX 20-NOV-2003.

XX 07-APR-2003; 2003US-00409772.

XX 07-JAN-1999; 99US-0115033P.

XX 07-JAN-2000; 2000US-00479614.

XX (MCCA/) MCCALL C.  
 XX (WEBE/) WEBER E.

XX McCall C, Weber E;

XX WPI; 2004-010802/01.

XX N-PSDB; ADG73236.

XX New isolated nucleic acid molecule encoding a portion of a feline IgE  
 XX heavy chain protein, useful for treating and/or eliciting feline immune  
 XX responses for IgE-mediated responses, such as allergies.

XX Claim 12; SEQ ID NO 14; 44pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a  
 XX portion of a feline IgE heavy chain protein. The methods and compositions  
 XX of the present invention are useful for eliciting feline immune responses  
 XX for and/or treating IgE-mediated responses, such as allergies. This is  
 XX the amino acid sequence of a cat immunoglobulin E (IgE) constant region.

XX Sequence 431 AA;

Query Match 100.0%; Score 97; DB 8; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGKQ 18  
 |||||  
 Db 151 VDGQKATNIFPYTAPGKQ 168

RESULT 3

ABP96580

ID ABP96580 standard; protein; 496 AA.

XX AC ABP96580;

XX 28-MAY-2003 (first entry)

XX Cat IgE heavy chain amino acid sequence SEQ ID NO:25.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
 XX immune response; major histocompatibility complex; MHC; immunogenic;  
 XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 XX dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 XX urticaria hives.

XX Felis catus.

XX W02003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) ICE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 XX against IgE, by identifying peptide eliciting CTL response to IgE  
 XX peptides naturally presented by major histocompatibility complex class I  
 XX protein.

XX Example 7; Page 145-147; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides  
 XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 XX E (IgE), comprising providing a test peptide (T) suspected of being able  
 XX to bind to major histocompatibility complex (MHC) class I molecule, and  
 XX evaluating (T) for ability to elicit in a mammal a CTL response to  
 XX naturally processed and presented IgE peptides, where a peptide that  
 XX induces such a response is identified. Also described are compositions:  
 XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 XX (C2) comprising at least one isolated polynucleotide encoding (I); and  
 XX (C3) comprising antigen-presenting cells that recognise at least one (I).  
 XX Where Cl-3 are able to bind to at least one MHC class I molecule and to  
 XX elicit in a mammal a CTL response to naturally processed and presented  
 XX IgE peptides. Cl-3 have antiallergic, antiasthmatic, immunosuppressive,  
 XX vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 XX and can be used as inducers of a CTL response against IgE, and in  
 XX vaccines. Cl-3 can be used for modulating an IgE-mediated condition in a  
 XX mammal. Cl-3 are useful for modulating an IgE-mediated condition such as  
 XX IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic  
 XX hypersensitivity condition, IgE myeloma in a mammal. Preferably, Cl-3 are  
 XX useful for treating atopic hypersensitivity conditions (such as allergic  
 XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 XX hives). The present sequence represents an IgE heavy chain amino acid  
 XX sequence, which is given in an example from the present invention

XX Sequence 496 AA;

Query Match 100.0%; Score 97; DB 6; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGKQ 18



```

Db      216 VDGQKATNIFPYTAPGKQ 233
|||||
RESULT 4
ABU09338
ID ABU09338 standard; protein; 496 AA.
XX
AC ABU09338;
XX
DT 27-JUN-2003 (first entry)
XX
DE Feline IgE epsilon heavy chain #2.
XX
KW Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
KW IgE-mediated immune response; allergy; neoplasia; vaccine technology;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
OS Felis catus.
XX
PN US2003013183-A1.
XX
PD 16-JAN-2003.
XX
PF 07-JAN-2000; 2000US-00479614.
XX
PR 07-JAN-1999; 99US-0115033P.
XX
PA (MCCA/) MCCALL C.
PA (WEBE/) WEBER E.
XX
PI McCall C, Weber E;
XX
DR WPI; 2003-391997/37.
DR N-PSDB; ABX95715.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
PS Claim 1; Page 37-39; 45pp; English.
XX
CC The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #2
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGQKATNIFPYTAPGKQ 18
|||||
Db      216 VDGQKATNIFPYTAPGKQ 233
|||||
RESULT 5
ABU09336
ID ABU09336 standard; protein; 496 AA.
XX
AC ABU09336;
XX
DT 27-JUN-2003 (first entry)
XX
DE Feline IgE epsilon heavy chain #1.
XX
KW Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
OS Felis catus.
XX
PN US2003013183-A1.
XX
PD 16-JAN-2003.
XX
PF 07-JAN-2000; 2000US-00479614.
XX
PR 07-JAN-1999; 99US-0115033P.
XX
PA (MCCA/) MCCALL C.
PA (WEBE/) WEBER E.
XX
PI McCall C, Weber E;
XX
DR WPI; 2003-391997/37.
DR N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
PS Claim 1; Page 24-25; 45pp; English.
XX
CC The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #1
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGQKATNIFPYTAPGKQ 18
|||||
Db      216 VDGQKATNIFPYTAPGKQ 233
|||||
RESULT 6
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
AC ADG73251;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cat partial immunoglobulin E (IgE) heavy chain #2.
XX
KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
KW immune response; IgE-mediated response; allergy; cat; heavy chain.

```

IgE-mediated immune response; allergy; neoplasia; vaccine technology; antibody technology; antiallergic; antiparasitic; cytostatic.

Felis catus.

Location/Qualifiers  
66..496  
/note= "This sequence is given as SEQ ID No:14 and is specifically claimed in Claim 12"  
284..309  
/note= "This sequence is given as SEQ ID No:11 and is specifically claimed in Claim 9"  
288..305  
/note= "This sequence is given as SEQ ID No:8 and is specifically claimed in Claim 10"  
291..302  
/note= "This sequence is given as SEQ ID No:5 and is specifically claimed in Claim 11"

US2003013183-A1.  
16-JAN-2003.  
07-JAN-2000; 2000US-00479614.  
07-JAN-1999; 99US-0115033P.  
(MCCA/) MCCALL C.  
(WEBE/) WEBER E.  
McCall C, Weber E;  
WPI; 2003-391997/37.  
N-PSDB; ABX95713.  
New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.  
Claim 1; Page 24-25; 45pp; English.

The present invention relates to the isolation of feline immunoglobulin E (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating feline IgE-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, small molecule/antibody technology, molecular biology, and various immunological techniques related to feline IgE and its functions. The present sequence represents feline IgE epsilon heavy chain #1

Sequence 496 AA;

Query Match 100.0%; Score 97; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPGKQ 18  
|||||  
Db 216 VDGQKATNIFPYTAPGKQ 233  
|||||

RESULT 6  
ADG73251  
ID ADG73251 standard; protein; 496 AA.  
XX  
AC ADG73251;  
XX

DT 11-MAR-2004 (first entry)  
XX  
DE Cat partial immunoglobulin E (IgE) heavy chain #2.

XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;  
KW immune response; IgE-mediated response; allergy; cat; heavy chain.



CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.

XX SQ Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAPG 16  
 |||||  
 DB 1 VDGQKATNIPFYTAPG 16

RESULT 9

AAV79995

ID AAY79995 standard; protein; 312 AA.

XX AC AAY79995;

XX DT 15-MAY-2000 (first entry)

XX DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Canis sp.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US013959.

XX PR 20-JUN-1998; 98US-00100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX PS WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 for immunization against allergy.

XX PS Example 1; Page 66-68; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 312 AA;

Query Match 89.7%; Score 87; DB 3; Length 312;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAPG 16  
 |||||  
 DB 48 VDGQKATNIPFYTAPG 63

RESULT 10

AAW23067

ID AAW23067 standard; protein; 417 AA.

XX AC AAW23067;

XX DT 30-JUN-2005 (revised)

XX DT 16-JUN-2005 (revised)

XX DT 19-FEB-1998 (first entry)

XX DE Canine IgE heavy chain constant region (exon 1-4 product).

XX KW IgE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX OS Canis familiaris.

XX FH Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX PN WO9730156-A2.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US002322.

XX PR 14-FEB-1996; 96US-00601197.

XX PA (IDEX-) IDEXX LAB INC.

XX PI Mermer B, Harris RA, Siefring AE;

XX PS WPI; 1997-425031/39.

XX PS N-PSDB; AAT79278.

XX PT Isolated canine IgE heavy chain constant region DNA - useful to develop  
 products for treatment of canine allergies and for immunomodulation in  
 dogs.

XX PS Disclosure; Page 35-39; 59pp; English.

XX CC This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE  
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat Type I immediate hypersensitivity, and for immunomodulation



Query Match	79.4%;	Score 77;	DB 6;	Length 577;
Best Local Similarity	77.8%;	Pred. No. 0.00049;		
Matches 14; Conservative	2;	Mismatches 2;	Indels 0;	Gaps 0;
ID	ADP90022	Standard, protein, 337 aa.		
XX	XX			
AC	ADF90022;			
XX	XX			
DT	26-FEB-2004	(first entry)		

```

XX      Opossum-rat chimeric IgE polypeptide.
DE
XX      IgE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;
KW      antiasthmatic; dermatological.
XX
XX      Chimeric.
OS
OS      Didelphis virginiana.
OS      Rattus sp.
XX
XX      WO2003096966-A2.
PN
XX
XX      27-NOV-2003.
PD
XX
XX      15-MAY-2003; 2003WO-IB002503.
PF
XX
XX      21-MAY-2002; 2002US-0382552P.
PR
XX      (RESI-) RESISTENTIA PHARM AB.
PA
XX      Lundgren M, Fuentes A, Magnusson A;
PI      WPI; 2004-042496/04.
XX
XX      N-PSDB; ADF90020, ADF90021.
DR
XX
XX      New host cell comprising a nucleic acid vector comprising a
PT      cytomegalovirus promoter, an Ig leader sequence, an insert sequence or
PT      SV40 late polyadenylation sequence, useful in producing a chimeric IgE
PT      polypeptide.
XX
XX      Claim 3; SEQ ID NO 3; 23pp; English.
XX
XX      The present sequence is the protein sequence of an opossum CH2-rat CH3-
CC      opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic
CC      acid encoding ORO can be used for recombinant production of this chimeric
CC      IgE in host, e.g. CHO, cells. The invention provides methods and
CC      materials related to expressing chimeric IgE proteins. Nucleic acid
CC      vectors, host cells, and methods for producing chimeric IgE polypeptides
CC      are provided. When administered to a mammal, the chimeric polypeptides
CC      can reduce the IgE antibody effects of IgE-related diseases such as
CC      asthma, allergies and eczema.
XX
XX      Sequence 337 AA;
SQ
      Query Match          61.9%; Score 60; DB 8; Length 337;
      Best Local Similarity 61.1%; Pred. No. 0.2;
      Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAPGKQ 18
      |||||:|:|||||:
DB      56 VDGQEAENLFYTTTPKX 73

Search completed: August 30, 2006, 04:22:05
Job time : 66.4545 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 10.7273 Seconds  
(without alignments)  
161.448 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97

Sequence: 1 VDGQKATNIPPYTAGPKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2	T16880
2	43	44.3	633	2	S62057
3	43	44.3	658	2	AH0110
4	42	43.3	381	2	AD2436
5	42	43.3	643	1	S15623
6	42	43.3	683	2	B71325
7	42	43.3	1032	2	S74487
8	42	43.3	1686	2	A87692
9	41	42.3	241	2	T17798
10	41	42.3	544	2	D88449
11	41	42.3	623	2	T22177
12	41	42.3	713	2	JE0230
13	41	42.3	2998	2	T49648
14	40.5	41.8	363	2	C82607
15	40.5	41.8	1371	2	D82666
16	40	41.2	101	2	G69203
17	40	41.2	109	2	F89886
18	40	41.2	179	2	D90167
19	40	41.2	227	2	C75582
20	40	41.2	240	2	C89967
21	40	41.2	242	1	LXBS
22	40	41.2	258	2	AF0306
23	40	41.2	327	2	S40753
24	40	41.2	374	2	G81926
25	40	41.2	391	2	T32714
26	40	41.2	419	2	C81179
27	40	41.2	454	2	AH2821
28	40	41.2	470	2	H97599
29	40	41.2	506	2	T07942

30 40 41.2 645 2 T16078 hypothetical prote  
31 40 41.2 812 2 T07745 phosphatidylinosit  
32 40 41.2 814 2 T07761 phosphatidylinosit  
33 40 41.2 831 2 T05265 coat protein gamma  
34 40 41.2 857 1 Q0BB1L glycoprotein B - h  
35 40 41.2 915 2 T12526 hypothetical prote  
36 40 41.2 1013 2 G71460 probable outer mem  
37 40 41.2 1064 2 T40751 isoleucyl-trna syn  
38 40 41.2 1203 2 T28895 hypothetical prote  
39 40 41.2 3069 2 H70656 fatty-acid synthas  
40 40 41.2 3076 2 A87058 fatty acid synthas  
41 39 40.2 157 2 A69637 transcription elon  
42 39 40.2 213 2 C64041 hypothetical prote  
43 39 40.2 308 2 H95965 hypothetical prote  
44 39 40.2 308 2 F95416 hypothetical prote  
45 39 40.2 374 2 G86267 T6J4.7 protein - A

ALIGNMENTS

RESULT 1

T16880  
hypothetical protein T14G12.4 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 05-Oct-2004  
C;Accession: T16880  
R;Wilcox, L.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid T14G12.  
A;Reference number: Z18596  
A;Accession: T16880  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-270 <WIL>  
A;Cross-references: UNIPROT:Q22510; UNIPARC:UPI00000075025; EMBL:U41268; NID:g1086843; PI  
C;Genetics:  
A;Gene: CESP:T14G12.4  
A;Introns: 37/1; 72/3; 164/1  
F;93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;  
Best Local Similarity 57.1%; Pred. No. 1.8;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GQKATNIPPYTAGP 16

Db 205 GAAGANLFFIFSPG 218

RESULT 2

S62057  
Proline-rich protein LAS17 - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein O4724; protein YOR181w  
C;Species: Saccharomyces cerevisiae  
C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: S62057; S67073  
R;Toh-e, A.  
submitted to the EMBL Data Library, December 1995  
A;Description: Yeast mutants sensitive to local anesthetics.  
A;Reference number: S62057  
A;Accession: S62057  
A;Molecule type: DNA  
A;Residues: 1-633 <TOH>  
A;Cross-references: UNIPROT:Q12446; UNIPARC:UPI0000003CA29; EMBL:D78487; NID:g1101756; PI  
R;Hughes, B.; Pohl, T.M.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S66685  
A;Accession: S67073  
A;Molecule type: DNA  
A;Residues: 1-633 <HUG>  
A;Cross-references: UNIPARC:UPI0000003CA29; EMBL:Z75089; NID:gl420436; PID:e252060; PID:g  
A;Experimental source: strain S288C

## C;Genetics:

A;Gene: SGD:LAS17  
A;Cross-references: SGD:S0005707; MIPS:YOR181w  
A;Map position: 15R

Query Match 44.3%; Score 43; DB 2; Length 633;  
Best Local Similarity 53.3%; Pred. No. 34;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QKATNIFPYTAPGKQ 18  
| ||| ||| : :  
Db 283 QSATNRPFPVPQQQ 297

## RESULT 3

AH0110  
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AH0110  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AH0110  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-658 <KUR>  
A;Cross-references: UNIPROT:Q8ZHU0; UNIPARC:UPI00000CD765; GB:AL590842; PIDN:CAC89747.1;  
C;Genetics:  
A;Gene: YPO0902

Query Match 44.3%; Score 43; DB 2; Length 659;  
Best Local Similarity 61.5%; Pred. No. 35;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VDQKATNIFPYT 13  
: ||||| :  
Db 99 LMGQKATNLAPAT 111

## RESULT 4

AD2436  
ATP-binding protein of polyamine ABC transporter all5044 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 31-Dec-2004  
C;Accession: AD2436  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AD2436  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-381 <KUR>  
A;Cross-references: UNIPROT:Q8VM92; UNIPARC:UPI00000CED3F; GB:BA0000019; PIDN:BAB76743.1;  
C;Genetics:  
A;Experimental source: strain PCC 7120  
A;Gene: all5044

Query Match 43.3%; Score 42; DB 2; Length 381;  
Best Local Similarity 53.3%; Pred. No. 29;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDQKATNIFPYTAP 15  
: ||||| :  
Db 80 IQGQPMTNIPYRRP 94

## RESULT 5

S15623  
E1 protein - human papillomavirus type 57  
C;Species: human papillomavirus type 57  
A;Note: host Homo sapiens (man)  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: S15623  
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M. Virus Res. 18, 81-98, 1990  
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 2b  
A;Reference number: S15614; MUID:91188699; PMID:1964523  
A;Accession: S15623  
A;Molecule type: DNA  
A;Residues: 1-643 <HIR>  
A;Cross-references: UNIPROT:P22153; UNIPARC:UPI000013813; EMBL:X55965; NID:G60882; PIDN  
C;Superfamily: papillomavirus E1 protein  
C;Keywords: early protein

Query Match 43.3%; Score 42; DB 1; Length 643;  
Best Local Similarity 53.8%; Pred. No. 51;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 KATNIFPYTAPGK 17  
| ||| ||| : :  
Db 581 KFTNRPFPASPG 593

## RESULT 6

B71325  
conserved hypothetical protein TP0421 - syphilis spirochete  
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: B71325  
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Swinerton, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDowell, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998  
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A;Reference number: A71250; MUID:98332770; PMID:9665876  
A;Accession: B71325  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-683 <COL>  
A;Cross-references: UNIPROT:O83436; UNIPARC:UPI00000COA71; GB:AE001220; GB:AE000520; NID  
A;Experimental source: strain Nichols  
C;Genetics:  
A;Gene: TP0421

Query Match 43.3%; Score 42; DB 2; Length 683;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYTAPG 16  
| ||| : : :  
Db 278 GQKSARFFGFSAPG 291

## RESULT 7

S74487  
hypothetical protein sl11060 - Synecchocystis sp. (strain PCC 6803)  
C;Species: Synecchocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S74487  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis sp.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S74487  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA



D88449

protein F54D8.3 [imported] - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: D88449  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: D88449  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-544 <STO>  
A;Cross-references: UNIPROT:Q20780; UNIPARC:UPI000174F99; GB:chr\_III; PIDN:AAA20615.1;  
C;Genetics:  
A;Gene: F54D8.3  
A;Map position: 3  
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match	42.3%	Score 41;	DB 2;	Length 544;
Best Local Similarity	44.4%	Pred. No. 63;		
Matches	8;	Conservative 3;	Mismatches 7;	Indels 0;
Gaps	0;			

Qy 1 VDGQKANNIFYTTPGKQ 18  
|||::| | | | |  
Db 389 VDGKQVETILKYIAGKK 406

RESULT 11  
T22177  
hypothetical protein F44F1.3 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*

A:Accession: T22177  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-623 <WIL>  
 A:Cross-references: UNIPROT:O02260; UNIPARC:UPI000017B9C4; EMBL:Z81083; PIDN:CAB03101.1;  
 A:Experimental source: clone F44F1  
 C:Genetics:  
 A:Gene: CESP:F44F1.3  
 A:Map position: 1  
 A:Introns: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3  
  
 Query Match 42.3%; Score 41; DB 2; Length 623;  
 Best Local Similarity 55.0%; Pred. No. 74;  
 Matches 11; Conservative 0; Mismatches 5; Indels 4; Gaps 1;  
  
 Qy 1 VDGQKATNI----FFYTAPG 16  
 ||||| | | |||||  
 Db 152 VDGQWKTIIDYFPYTDG 171  
  
 RESULT 12  
 JEO230  
 NADPH-cytochrome P450 oxidoreductase (EC 1.-.-.-) - common tobacco  
 C:Species: Nicotiana tabacum (common tobacco)  
 C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
 C:Accession: JEO230  
 F:Yamada, T.; Imaishi, H.; Oka, A.; Ohkawa, H.  
 Biosci. Biotechnol. Biochem. 62, 1403-1411, 1998  
 A:Title: Molecular cloning and expression in Saccharomyces cerevisiae of tobacco NADPH-c  
 A:Reference number: JEO230; MUID:98386693; PMID:9720224  
 A:Accession: JEO230  
 A:Molecule type: mRNA  
 A:Residues: 1-713 <YAM>  
 A:Cross-references: UNIPROT:Q7M275; UNIPARC:UPI0000175049

A:Cross8-references: UNIPROT:Q7M275; UNIPARC:UPI0000175049

C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase  
 C;Keywords: flavoprotein; oxidoreductase  
 F;107-712/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
 F;109-257/Domain: flavodoxin homology <PLX>

Query Match 42.3%; Score 41; DB 2; Length 713;  
 Best Local Similarity 57.1%; Pred. No. 85;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQKATNIPFYTA 14  
 :||| ||| |||  
 Db 265 LGGDDATRAATPYTA 278

## RESULT 13

T49648  
 hypothetical protein B8B20.20 [imported] - Neurospora crassa  
 C;Species: Neurospora crassa  
 C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
 C;Accession: T49648  
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000  
 A;Reference number: Z25022  
 A;Accession: T49648  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-2298 <SCH>  
 A;Cross-references: UNIPROT:Q96U00; UNIPARC:UPI000017B4BA; EMBL:AL355933; GSPDB:GN00116;  
 A;Experimental source: BAC clone B8B20; strain OR74A  
 C;Genetics:  
 A;Gene: NCSP:B8B20.20  
 A;Map position: 6  
 A;Introns: 426/3

Query Match 42.3%; Score 41; DB 2; Length 2298;  
 Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QKATNIPFYTAGK 17  
 : : ||| |||  
 Db 1694 ERVTQVLPLYFQPGK 1707

## RESULT 14

C82607  
 DNA primase XF2025 [imported] - Xylella fastidiosa (strain 9a5c)  
 C;Species: Xylella fastidiosa  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: C82607  
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
 Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A;Reference number: A82515; MUID:20365717; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below  
 A;Accession: C82607  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-363 <STM>  
 A;Cross-references: UNIPROT:Q9P6W0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID  
 A;Experimental source: strain 9a5c  
 R;Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328

A;Contents: annotation  
 C;Genetics:  
 A;Gene: XF2025

Query Match 41.8%; Score 40.5; DB 2; Length 363;  
 Best Local Similarity 55.6%; Pred. No. 49;  
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQKATNIPFYTAGKQ 18  
 :||| ||| ||| |||  
 Db 284 VDG---TAFPPFAPGGEQ 298

## RESULT 15

D82606  
 DNA primase XF2061 [imported] - Xylella fastidiosa (strain 9a5c)  
 C;Species: Xylella fastidiosa  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: D82606  
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
 Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A;Reference number: A82515; MUID:20365717; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below  
 A;Accession: D82606  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1371 <SIM>  
 A;Cross-references: UNIPROT:Q9PBS8; UNIPARC:UPI00000C290E; GB:AE004022; GB:AE003849; NID  
 A;Experimental source: strain 9a5c  
 R;Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328  
 A;Contents: annotation  
 C;Genetics:  
 A;Gene: XF2061

Query Match 41.8%; Score 40.5; DB 2; Length 1371;  
 Best Local Similarity 55.6%; Pred. No. 2.2e+02;  
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQKATNIPFYTAGKQ 18  
 :||| ||| ||| |||  
 Db 1292 VDG---TAFPPFAPGGEQ 1306

Search completed: August 30, 2006, 04:30:56  
 Job time : 11:7273 secs

RESULT 2	Q8R6B3_FUSNN	Q8R6B3_FUSNN	PRELIMINARY;	PRT;	382 AA.
ID	Q8R6B3_FUSNN	Q8R6B3_FUSNN	PRELIMINARY;	PRT;	382 AA.
AC	Q8R6B3_FUSNN	Q8R6B3_FUSNN	PRELIMINARY;	PRT;	382 AA.
DT	01-JUN-2002,	integrated into UniProtKB/TrEMBL.			
DT	01-JUN-2002,	sequence version 1.			
DT	07-FEB-2006,	entry version 16.			
DE	(R) -2-hydroxyglutaryl-CoA dehydratase	beta-subunit (EC 4.2.1.-).			
GN	OrderedLocusNames=FN208;				
OS	Fusobacterium nucleatum subsp. nucleatum.				
OC	Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;				

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OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 25586;
RX MEDLINE=11886394; PubMed=11889109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapattal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
CC -----
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CC -----
DR EMBL; AE009951; AAL94414.1; -; Genomic_DNA.
DR BioCyc; FNUC190304:FN0208-MONOMER; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 9.1;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGKATNIFPYTAP 15
Db 28 EGKKAIGFPPYAP 41

RESULT 3
Q95QA9_CABEL
ID Q95QA9_CABEL PRELIMINARY; PRT; 168 AA.
AC Q95QA9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Forkhead transcription factor family protein 2, isoform b.
GN Name=fkh-2; ORFNames=Ti4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- INTERACTION:
CC Q9XW88:php-3; NbExp=1; IntAct=EBI-327741, EBI-316766;
CC Q21648:RO2F2.5; NbExp=1; IntAct=EBI-327741, EBI-314179;
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U41268; AAA82436.1; -; Genomic_DNA.
DR PIR; T16880; T16880.
DR HSSP; Q99958; IDS5.
DR SMR; Q22510; 93-170.
DR IntAct; Q22510; -.
DR WormBase; WBGene00001434; fkh-2.
DR WormPep; T14G12.4a; CE04965.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK HEAD 1; 1.
DR PROSITE; PS00658; FORK HEAD 2; 1.
DR PROSITE; PS00039; FORK HEAD 3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 270 AA; 30491 MW; 7C491165EC76175 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00658; FORK HEAD 2; 1.
DR PROSITE; PS00039; FORK HEAD 3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4E69968572 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYTAPG 16
Db 103 GAAANLFPYFSPG 116

RESULT 4
Q22510_CABEL
ID Q22510_CABEL PRELIMINARY; PRT; 270 AA.
AC Q22510;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 39.
DE Forkhead transcription factor family protein 2, isoform a.
GN Name=fkh-2; ORFNames=Ti4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- INTERACTION:
CC Q9XW88:php-3; NbExp=1; IntAct=EBI-327741, EBI-316766;
CC Q21648:RO2F2.5; NbExp=1; IntAct=EBI-327741, EBI-314179;
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -----
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CC -----
DR EMBL; U41268; AAA82436.1; -; Genomic_DNA.
DR PIR; T16880; T16880.
DR HSSP; Q99958; IDS5.
DR SMR; Q22510; 93-170.
DR IntAct; Q22510; -.
DR WormBase; WBGene00001434; fkh-2.
DR WormPep; T14G12.4a; CE04965.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK HEAD 1; 1.
DR PROSITE; PS00658; FORK HEAD 2; 1.
DR PROSITE; PS00039; FORK HEAD 3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 270 AA; 30491 MW; 7C491165EC76175 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```

QY 3 GQKATNIFPYTPAG 16
D 205 GAAANLFPYFSPG 218
| | | | |
| | | | |
| | | | |

RESULT 5
Q3N7V1_9PROT PRELIMINARY; PRT; 1143 AA.
AC Q3N7V1;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Putative type 4 fibrial biogenesis protein Pily1 precursor.
GN ORFNames=NEUTDRAFT_0559;
OS Nitrosomonas eutropha C71.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OX Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=335283;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C71;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israeli S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Nitrosomonas eutropha
RT C71.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C71;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RA "Annotation of the draft genome assembly of Nitrosomonas eutropha
RT C71.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
KW Signal.
SQ SEQUENCE 1143 AA; 123766 MW; 9C270A88F6A0FAF1 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 1143;
Best Local Similarity 64.3%; Pred. No. 95;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 DGOKATNIFPYTPAP 15
D 383 DGSKLTNHFNTSP 396
| | | | |
| | | | |
| | | | |

RESULT 6
Q36VF1_RHOPA PRELIMINARY; PRT; 365 AA.
AC Q36VF1;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=RPEDRAFT_0215;
OS Rhodopseudomonas palustris BisA53.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=316055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BisA53;

QY 3 GQKATNIFPYTPAG 16
D 205 GAAANLFPYFSPG 218
| | | | |
| | | | |
| | | | |

RESULT 7
Q608X6_METCA PRELIMINARY; PRT; 1054 AA.
AC Q608X6;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hydrophobe/amphiphile Efflux-1 (HAE1) family protein.
GN OrderedLocNames=MCA1360;
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
OX NCBI_TaxID=414;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bath / NCIMB 11132;
RX PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
RA Ward N.L., Larsen O., Sakwa J., Bruseth L., Khouri H.M., Durkin A.S.,
RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,
RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA Grindhaug S.H., Holt I.E., Eichhammer I., Jonassen I., Vanaken S.,
RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
RA Eisen J.A.;
RA "Genomic insights into methanotrophy: the complete genome sequence of
RT Methylococcus capsulatus (Bath).";
RL PLoS Biol. 2:1616-1628(2004).
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CC -----
EMBL; A017282; AAU92574.1; -; Genomic_DNA.
DR TIGR; MCA1360; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001036; Acrflvin_res.
DR InterPro; IPR004764; HAE1.

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DR Pfam; PF00873; ACR_tran; 1.
DR PRINTS; PR00702; ACRIFAVINRP.
DR TIGRFAMs; TIGR00915; 2A0602; 1.
KW Complete proteome.
SQ SEQUENCE 1054 AA; 115005 MW; BB032CB91B38D1A8 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1054;
Best Local Similarity 56.2%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPG 16
Db 294 VNGHKSTQIVVYTLPG 309

RESULT 8
Q94H26 ORYSA PRELIMINARY; PRT; 1538 AA.
AC Q94H26;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 18.
DE Putative gag-pol polyprotein.
GN Name=OSJNBa0077G22.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Qiyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
RA Uterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RA "Oryza sativa chromosome 3 BAC OSJNBa0077G22 genomic sequence.";
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AC084831; AAK52152.1; -; Genomic_DNA.
DR Gramene; Q94H26; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0015074; P:DNA integration; IEA.
DR InterPro; IPR005162; Retrotrans gag.
DR InterPro; IPR008916; Retrov capsid_C.
DR InterPro; IPR002156; RNase_H.
DR InterPro; IPR001584; Rve.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF06665; rve; 1.
DR PROSITE; PS00994; INTEGRASE; 1.
DR PROSITE; PS00879; RNASE_H; 1.
KW Polyprotein.
SQ SEQUENCE 1538 AA; 174629 MW; 5E7A521B398BC776 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1538;
Best Local Similarity 61.5%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYT 13
Db 740 VDGRAAVNLMPYT 752

RESULT 9

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Q565U8_9BACT PRELIMINARY; PRT; 408 AA.
AC Q565U8;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE 3-oxoacyl-CoA thiolase.
GN ORFNames=fc62;
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15997700; DOI=10.1016/j.syapm.2005.02.006;
RA Kube M., Beck A., Meyerderks A., Amann R., Reinhardt R., Rabus R.;
RT "A catabolic gene cluster for anaerobic benzoate degradation in
methanotrophic microbial Black Sea mats.";
RL Syst. Appl. Microbiol. 28:287-294(2005).
CC -|- SIMILARITY: Belongs to the thiolase family.
CC
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CC
DR EMBL; CR931837; CAI78864.1; -; Genomic_DNA.
DR InterPro; IPR002155; Thiolase.
DR PANTHER; PTHR18919; Thiolase; 2.
DR Pfam; PF02803; Thiolase_C; 1.
DR Pfam; PF00108; Thiolase_N; 1.
DR TIGRFAMs; TIGR01930; AcCoA-C-Actrans; 1.
DR PROSITE; PS00737; THIOLEASE 2; 1.
SQ SEQUENCE 408 AA; 43389 MW; F9BECC546AF32193 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 408;
Best Local Similarity 38.9%; Pred. No. 70;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGKQ 18
Db 45 IDASIGANVYQFTAPGAQ 62

RESULT 10
Q2L2W7 BORAV PRELIMINARY; PRT; 491 AA.
AC Q2L2W7;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DT 07-MAR-2006, entry version 1.
DE Putative phage portal protein.
GN ORFNames=BAV1315; 197N.
OS Bordetella avium 197N.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=360910;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=197N;
RA Sebaihia M.;
RT "The genome sequence of the poultry pathogen Bordetella avium, and
genomic comparisons with related species infecting mammals.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AM167904; CAJ48922.1; -; Genomic DNA.
SQ SEQUENCE 491 AA; 54500 MW; E900B690162C1AA4 CRC64;

Query Match 46.9%; Score 45.5; DB 2; Length 491;
Best Local Similarity 47.6%; Pred. No. 1e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

Qy 3 GQKATNIF-----PVTAPG 16

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Db      30 GEARNLFFVMTFFQPYGAPG 50
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RESULT 11
Q619H6 CAEBR PRELIMINARY; PRT; 279 AA.
AC Q619H6;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Hypothetical protein CBG14280.
GN Name=CBG14280;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M.,
RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of Caenorhabditis briggsae: a platform for
RT comparative genomics.";
RL PLoS Biol. 1:166-192(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC -----
DR EMBL; CAAC0100068; CAB68479.1; -; Genomic_DNA.
DR SMR; Q619H6; 101-178.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Hypothetical protein; Nuclear protein;
KW Transcription; Transcription regulation.
SQ SEQUENCE 279 AA; 31322 MW; 0C926B95AD122D9B CRC64;

Query Match 46.4%; Score 45; DB 2; Length 279;
Best Local Similarity 57.1%; Pred. No. 69;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYTAPG 16
Db 213 GAAANLFFPYFNPNG 226
||:|:|:|
||:|:|:|

RESULT 12
ALN_STRCO STANDARD; PRT; 445 AA.
ID -ALN_STRCO
AC Q9RKU5;
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.

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DT 01-MAY-2000, sequence version 1.
DT 07-MAR-2006, entry version 37.
DE Probable allantoinase (EC 3.5.2.5).
GN OrderedLocusNames=SCO6247; ORFNames=SCAH10.12, STAH10.12;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=A3(2) / M145;
RX MEDLINE=1996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- CATALYTIC ACTIVITY: (S)-allantoin + H(2)O = allantoinate.
CC -!- COFACTOR: Zinc (By similarity).
CC -!- PATHWAY: Degradation of allantoin (purine catabolism); first step.
CC -!- SIMILARITY: Belongs to the DHOase family.
CC -----
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CC -----
DR EMBL; AL939126; CAB60166.1; -; Genomic_DNA.
DR HSSP; P81006; 1GKR.
DR GenomeReviews; AL645882 GR; SCO6247.
DR BioCyc; SCO61902:SCO6247-MONOMER; -.
DR InterPro; IPR006680; Amidohydro_1.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD000518; DHOase; 1.
KW Complete proteome; Hydrolase; Hypothetical protein; Metal-binding;
KW Purine metabolism; Zinc.
FT CHAIN 1 445 Probable allantoinase.
FT METAL 63 63 /FTID=PRO_0000165943.
FT METAL 65 65 Zinc (Potential).
SQ SEQUENCE 445 AA; 47492 MW; 75955C5F98632570 CRC64;

Query Match 46.4%; Score 45; DB 1; Length 445;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDGKATNIFPYTAP 15
Db 26 VTGEKITAVLPYDAP 40
||:|:|:|
||:|:|:|

RESULT 13
Q41FN3 GIBZE PRELIMINARY; PRT; 811 AA.
AC Q41FN3;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=FG03975.1;
OC Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PH-1 / NRRL 31084;

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RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Fato S., Ferreira P., FitzGerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A.,
RA Karatas A., Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J.,
RA Meneus L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Purcell S., Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schupack R., Seaman S., Severy P.,
RA Smirnov S., Smith C., Spencer B., Stubbach-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Teafaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AACW01000168; EAA73443.1; -; Genomic_DNA.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 1.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 811 AA; 84248 MW; C3C5A4A02E10DA79 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 811;
Best Local Similarity 58.8%; Pred.No. 2.1e+02;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 DGQKATNIFPYTPAGKQ 18
DB 676 DDDKETATGGYTPAGKQ 692

RESULT 14
ID Q2ZH01 CALSA PRELIMINARY; PRT; 908 AA.
AC Q2ZH01_
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Conserved membrane protein.
DE ORFNames=CgacDRAFT_0884;
OS Caldicellulosiruptor saccharolyticus DSM 8903.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
OC Caldicellulosiruptor.
OX NCBI_TaxID=351627;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 8903;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Caldicellulosiruptor
RT saccharolyticus DSM 8903.";
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RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=DSM 8903;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Caldicellulosiruptor
RA saccharolyticus DSM 8903.";
RT Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AALW01000031; EAP42636.1; -; Genomic_DNA.
DR EMBL; AALW01000031; EAP42636.1; -; Genomic_DNA.
SQ SEQUENCE 908 AA; 105151 MW; B5E42A7161E5ED12 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 908;
Best Local Similarity 38.9%; Pred.No. 2.4e+02;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTPAGKQ 18
DB 576 LDGYTKNYYPYSEPTEE 593

RESULT 15
ID GAGC1 HUMAN STANDARD; PRT; 102 AA.
AC O60823;
DT 11-JAN-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 36.
DE G antigen family C 1 protein (Prostate-associated gene 4 protein)
DE (PAGE-4) (PAGE-1) (GAGE-9).
DE Name=PAGE4; Synonyms=GAGEC1; ORFNames=JM27;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA]
RX MEDLINE=98393718; PubMed=9724777; DOI=10.1073/pnas.95.18.10757;
RA Brinkmann U., Vasmatazis G., Lee B., Yerushalmi N., Essand M.,
RA Pastan I.;
RT "PAGE-1, an X chromosome-linked GAGE-like gene that is expressed in
RT normal and neoplastic prostate, testis, and uterus.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10757-10762(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Strom T.M., Nyakatura G., Hellebrand H., Drescher B., Rosenthal A.,
RA Meindl A.;
RT "Transcription map in Xp11.23.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15772651; DOI=10.1038/nature03440;
RA Moss M.T., Grafham D.V., Coffey A.J., Scherer S., McKay K., Muzny D.,
RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA Jones M.C., Hurler M.E., Andrews T.D., Scott C.E., Searle S., Chen R.,
RA Rameser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,
RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhy S.,
RA Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,
RA Barker G.B., Barlow K.F., Barrett I.P., Bates K.N., Beards D.M.,
RA Beasley H., Beasley O., Beck A., Bethel G., Blechnschmidt K., Brady N.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
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RA Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,  
RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,  
RA Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chinault C.,  
RA Cleric-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,  
RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,  
RA Delgado O., Deshazo D., Dhami P., Ding Y., Dinh H., Dodsworth S.,  
RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,  
RA Bades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,  
RA Faulkner L., Francis F., Frankland J., Fraser A.E., Gaiagoczy P.,  
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,  
RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,  
RA Hawes A., Heath P.D., Heilmann K., Hennig S., Hernandez J.,  
RA Hinzmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,  
RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,  
RA De Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,  
RA Kioschis P., Klages S., Knights A.J., Koslura A., Kovar-Smith C.,  
RA Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,  
RA Lloyd C., Lloyd D.M., Loulsegod H., Loveland J.E., Lovell J.D.,  
RA Lozado R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,  
RA McDowell J., McLaren S., McMurray A., Meidl P., Meitinger T.,  
RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,  
RA Mullikin J.C., Nguyen N., Nordstiek G., Nyakatura G., O'dell C.N.,  
RA Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,  
RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,  
RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,  
RA Ridler K.A., Schlesinger D., Schueler M.G., Sehra H.K.,  
RA Shaw-Smith C., Shen H., Sheridan E.M., Showkneen R., Skuce C.D.,  
RA Smith M.L., Socheran E.C., Steingruber H.E., Steward C.A., Storey R.,  
RA Swann R.M., Swarbrick D., Tabor P.E., Taudien S., Taylor T.,  
RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,  
RA Tromans A.C., d'Urso M., Verdusco D., Villasana D., Waldron L.,  
RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,  
RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,  
RA Williams G., Williams L., Williamson A., Williamson H., Wilming L.,  
RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,  
RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,  
RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,  
RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,  
RA Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,  
RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.,  
RT "The DNA sequence of the human X chromosome."  
RL Nature 434:325-337(2005).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Unknown.  
CC -!- TISSUE SPECIFICITY: Preferentially expressed in normal male and  
CC female reproductive tissues, prostate, testis, fallopian tube,  
CC uterus, and placenta, as well as in prostate cancer, testicular  
CC cancer, and uterine cancer.  
CC -!- SIMILARITY: Belongs to the GAGE family.

CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR ENBL; AF275258; AAF88037.1; -; mRNA.  
DR ENBL; AJ005894; CAA06751.1; -; mRNA.  
DR ENBL; AP238380; -; NOT ANNOTATED CDS; Genomic\_DNA.  
DR ENBL; BC010897; AH10897.1; -; mRNA.  
DR EnsEmbl; ENSG00000101951; Homo sapiens.  
DR H-InVDB; HIX0016804; -.  
DR HGNC; HGNC:4108; PAGE4.  
DR MIM; 300287; Gene.  
DR LinkHub; O60829; -.  
DR InterPro; IPR008625; GAGE.  
DR PANTHER; PTHR14047; GAGE; 1.  
DR Pfam; PF05831; GAGE; 1.  
FT CHAIN 1 102 G antigen family C 1 protein.  
FT /FTId=PRO 0000148348.  
SQ SEQUENCE 102 AA; 11153 MW; CE5D07AFBF73301B CRC64;  
Query Match 45.4%; Score 44; DB 1; Length 102;  
Best Local Similarity 43.8%; Pred. No. 35;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 2 DGQKATNIPYTPAGK 17  
DB 14 DGQEPDVVAFVAPGE 29  
||||| : : |||:  
Search completed: August 30, 2006, 04:29:18  
Job time : 72.1818 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 17.8182 Seconds  
(without alignments)  
88.424 Million cell updates/sec

Title: US-10-758-165a-10

Perfect score: 97

Sequence: 1 VDGQKATNIPFYTAGKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	97	100.0	431	2	US-09-479-614-14
2	97	100.0	496	2	US-09-479-614-2
3	97	100.0	496	2	US-09-479-614-29
4	87	89.7	108	2	US-09-281-760E-35
5	87	89.7	312	2	US-09-701-623C-2
6	87	89.7	426	1	US-08-336-583-2
7	87	89.7	426	5	PCT-US95-13795-2
8	77	79.4	343	2	US-09-401-636-7
9	60	61.9	341	2	US-09-401-636-3
10	60	61.9	341	2	US-09-401-636-4
11	60	61.9	341	2	US-09-401-636-6
12	60	61.9	341	2	US-09-401-636-9
13	60	61.9	341	2	US-09-401-636-11
14	60	61.9	342	2	US-09-401-636-5
15	60	61.9	342	2	US-09-401-636-8
16	60	61.9	345	2	US-09-401-636-10
17	42	43.3	449	2	US-09-252-991A-28547
18	42	43.3	985	2	US-09-933-777-6
19	42	43.3	985	2	US-09-933-777-66
20	42	43.3	985	2	US-09-934-064-6
21	42	43.3	985	2	US-09-994-064-66
22	42	43.3	985	5	PCT-US96-03916-6
23	42	43.3	985	5	PCT-US96-03916-66
24	41	42.3	135	2	US-09-252-991A-30004
25	41	42.3	232	2	US-09-489-039A-8106
26	41	42.3	497	2	US-10-077-699C-5

27 40 41.2 63 2 US-09-612-402B-29 Sequence 29, Appl  
28 40 41.2 63 2 US-09-542-520-29 Sequence 29, Appl  
29 40 41.2 242 2 US-09-286-690-8 Sequence 8, Appl  
30 40 41.2 391 2 US-09-721-870-38 Sequence 38, Appl  
31 40 41.2 503 2 US-09-147-009-11 Sequence 11, Appl  
32 40 41.2 505 2 US-09-612-402B-17 Sequence 17, Appl  
33 40 41.2 505 2 US-09-542-520-17 Sequence 17, Appl  
34 40 41.2 659 2 US-09-248-796A-24809 Sequence 24809, A  
35 40 41.2 829 2 US-10-197-220-169 Sequence 169, App  
36 40 41.2 829 2 US-10-055-364-46 Sequence 46, Appl  
37 40 41.2 854 2 US-09-350-841A-1589 Sequence 1589, Ap  
38 40 41.2 856 2 US-08-486-099-103 Sequence 103, App  
39 40 41.2 856 2 US-08-484-223B-103 Sequence 103, App  
40 41.2 856 2 US-08-919-597-103 Sequence 103, App  
41 40 41.2 856 2 US-08-475-668A-103 Sequence 103, App  
42 40 41.2 856 2 US-08-485-551A-103 Sequence 103, App  
43 40 41.2 856 2 US-08-471-913A-103 Sequence 103, App  
44 40 41.2 856 2 US-08-485-264A-103 Sequence 103, App  
45 40 41.2 856 2 US-08-474-349A-103 Sequence 103, App

#### ALIGNMENTS

RESULT 1  
US-09-479-614-14  
; Sequence 14, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
; ORGANISM: Felis catus

US-09-479-614-14

Query Match 100.0%; Score 97; DB 2; Length 431;  
Best Local Similarity 100.0%; Pred. No. 9e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGKQ 18  
Db 151 VDGQKATNIPFYTAGKQ 168

RESULT 2  
US-09-479-614-2  
; Sequence 2, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus

US-09-479-614-2

Query Match 100.0%; Score 97; DB 2; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIPFYTAGKQ 18  
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 Db 216 VDGOKATNIPFYTAGKQ 233

RESULT 3

US-09-479-614-29  
 ; Sequence 29, Application US/09479614  
 ; Patent No. 6573372  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCall, Catherine  
 ; APPLICANT: Weber, Eric  
 ; TITLE OF INVENTION: Peline Immunoglobulin E Molecules and Related Methods  
 ; FILE REFERENCE: P-1047  
 ; CURRENT APPLICATION NUMBER: US/09/479,614  
 ; CURRENT FILING DATE: 2000-01-07  
 ; EARLIER APPLICATION NUMBER: 60/115,033  
 ; EARLIER FILING DATE: 1999-01-07  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 29  
 ; LENGTH: 496  
 ; TYPE: PRT  
 ; ORGANISM: Felis catus  
 US-09-479-614-29

Query Match 100.0%; Score 97; DB 2; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIPFYTAGKQ 18  
 |||||  
 Db 216 VDGOKATNIPFYTAGKQ 233

RESULT 4

US-09-281-760E-35  
 ; Sequence 35, Application US/09281760E  
 ; Patent No. 6734287  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lawton, Robert  
 ; APPLICANT: Mermer, Brian  
 ; APPLICANT: Francoeur, Greg  
 ; TITLE OF INVENTION: Specific Binding Protein for Treating  
 ; TITLE OF INVENTION: Canine Allergy  
 ; FILE REFERENCE: 01-1275A  
 ; CURRENT APPLICATION NUMBER: US/09/281,760E  
 ; CURRENT FILING DATE: 1999-03-30  
 ; PRIOR APPLICATION NUMBER: 09/058,331  
 ; PRIOR FILING DATE: 1998-04-09  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 35  
 ; LENGTH: 108  
 ; TYPE: PRT  
 ; ORGANISM: Canis familiaris  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (81)..(81)  
 ; OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,  
 ; OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (82)..(82)  
 ; OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature

; LOCATION: (136)..(136)  
 ; OTHER INFORMATION: "n" stands for any nucleic acid  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (413)..(414)  
 ; OTHER INFORMATION: "n" stands for any nucleic acid  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (451)..(451)  
 ; OTHER INFORMATION: "n" stands for any nucleic acid  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (460)..(462)  
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 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (500)..(500)  
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 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (530)..(530)  
 ; OTHER INFORMATION: "n" stands for any nucleic acid  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (568)..(568)  
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 ; LOCATION: (847)..(849)  
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 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (853)..(853)  
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 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1382)..(1382)  
 ; OTHER INFORMATION: "n" stands for any nucleic acid  
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 ; NAME/KEY: misc feature  
 ; LOCATION: (1832)..(1832)  
 ; OTHER INFORMATION: "n" stands for any nucleic acid  
 US-09-281-760E-35

Query Match 89.7%; Score 87; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIPFYTAGP 16  
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 Db 47 VDGOKATNIPFYTAGP 62

RESULT 5

US-09-701-623C-2  
 ; Sequence 2, Application US/09701623C  
 ; Patent No. 681782  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang Ph.D., Chang Yi  
 ; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
 ; TITLE OF INVENTION: ALLERGY  
 ; FILE REFERENCE: 11514153U1  
 ; CURRENT APPLICATION NUMBER: US/09/701,623C  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13959  
 ; PRIOR FILING DATE: 1999-06-21  
 ; PRIOR APPLICATION NUMBER: 09/100,287  
 ; PRIOR FILING DATE: 1998-06-20  
 ; NUMBER OF SEQ ID NOS: 91  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 312  
 ; TYPE: PRT

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; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2

Query Match      89.7%; Score 87; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGP 16
Db      48 VDGQKATNIPFYTAGP 63
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RESULT 6
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5628415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match      89.7%; Score 87; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGP 16
Db      146 VDGQKATNIPFYTAGP 161
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RESULT 7
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match      89.7%; Score 87; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGP 16
Db      146 VDGQKATNIPFYTAGP 161
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RESULT 8
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-7

Query Match      79.4%; Score 77; DB 2; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00013;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
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Db      61 VDGQAEENLFPYTPPKR 78
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; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPPKR 79

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPPKR 79

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPPKR 79

RESULT 10
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPPKR 79

RESULT 11
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
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**This Page Blank (uspto)**



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 90.9091 Seconds  
(without alignments)  
91.717 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDGQKATNIPFYTAGKQ 18

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10
2	97	100.0	431	3	US-09-479-614-14
3	97	100.0	431	4	US-10-409-772-14
4	97	100.0	496	3	US-09-479-614-2
5	97	100.0	496	4	US-09-479-614-29
6	97	100.0	496	4	US-10-214-524-25
7	97	100.0	496	4	US-10-409-772-2
8	97	100.0	496	4	US-10-409-772-29
9	87	89.7	18	5	US-10-758-165-9
10	87	89.7	312	5	US-10-723-207-2
11	87	89.7	426	4	US-10-214-524-28
12	77	79.4	343	3	US-09-401-636-7
13	77	79.4	343	4	US-10-176-664-7
14	77	79.4	343	4	US-10-673-594-7
15	77	79.4	577	4	US-10-214-524-29
16	60	61.9	337	4	US-10-438-794-3
17	60	61.9	337	4	US-10-453-915-3
18	60	61.9	338	4	US-10-438-794-6
19	60	61.9	338	4	US-10-453-915-6
20	60	61.9	341	3	US-09-401-636-3
21	60	61.9	341	3	US-09-401-636-4
22	60	61.9	341	3	US-09-401-636-6
23	60	61.9	341	3	US-09-401-636-9
24	60	61.9	341	3	US-09-401-636-11
25	60	61.9	341	4	US-10-176-664-3
26	60	61.9	341	4	US-10-176-664-4
27	60	61.9	341	4	US-10-176-664-6

28	60	61.9	341	4	US-10-176-664-9	Sequence 9, Appli
29	60	61.9	341	4	US-10-176-664-11	Sequence 11, Appli
30	60	61.9	341	4	US-10-673-594-3	Sequence 3, Appli
31	60	61.9	341	4	US-10-673-594-4	Sequence 4, Appli
32	60	61.9	341	4	US-10-673-594-6	Sequence 6, Appli
33	60	61.9	341	4	US-10-673-594-9	Sequence 9, Appli
34	60	61.9	341	4	US-10-673-594-11	Sequence 11, Appli
35	60	61.9	342	3	US-09-401-636-5	Sequence 5, Appli
36	60	61.9	342	3	US-09-401-636-8	Sequence 8, Appli
37	60	61.9	342	4	US-10-176-664-5	Sequence 5, Appli
38	60	61.9	342	4	US-10-176-664-8	Sequence 8, Appli
39	60	61.9	342	4	US-10-673-594-5	Sequence 5, Appli
40	60	61.9	342	4	US-10-673-594-8	Sequence 8, Appli
41	60	61.9	345	3	US-09-401-636-10	Sequence 10, Appli
42	60	61.9	345	4	US-10-176-664-10	Sequence 10, Appli
43	60	61.9	345	4	US-10-673-594-10	Sequence 10, Appli
44	60	61.9	347	4	US-10-438-794-14	Sequence 14, Appli
45	60	61.9	347	4	US-10-453-915-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1

US-10-758-165-10  
; Sequence 10, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-10

Query Match 100.0%; Score 97; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGKQ 18  
| | | | | | | | | | | | | | | |  
Db 1 VDGQKATNIPFYTAGKQ 18

RESULT 2

US-09-479-614-14  
; Sequence 14, Application US/09479614  
; Publication No. US20030013183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catharine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-14

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Query Match      100.0%; Score 97; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      151 VDGQKATNIPFYTAGKQ 168

RESULT 3
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; EARLIER APPLICATION NUMBER: 60/115,033
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match      100.0%; Score 97; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      151 VDGQKATNIPFYTAGKQ 168

RESULT 4
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match      100.0%; Score 97; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 5
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
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; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match      100.0%; Score 97; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 6
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1-1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match      100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 7
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
Query Match      100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 8
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
Query Match      100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 9
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9
Query Match      89.7%; Score 87; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGK 16
Db      1 VDGQKATNIPFYTAGK 16

RESULT 10
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2
Query Match      89.7%; Score 87; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      48 VDGQKATNIPFYTAGP 63

RESULT 11
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Sway-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
Query Match      89.7%; Score 87; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      1 VDGQKATNIPFYTAGP 16
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Db      146 VDGQKATNIPFYTAGK 161

RESULT 12
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-7

Query Match      79.4%; Score 77; DB 3; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
      ||||| :||| :|
Db      61 VDGQKAENLFFYTAPPKR 78

RESULT 13
US-10-176-664-7
; Sequence 7, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match      79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
      ||||| :||| :|
Db      61 VDGQKAENLFFYTAPPKR 78

RESULT 14
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
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; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match      79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
      ||||| :||| :|
Db      61 VDGQKAENLFFYTAPPKR 78

RESULT 15
US-10-214-524-29
; Sequence 29, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICE-00101.P.1-1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Duckbilled platypus (Ornithorhynchus anatinus)
US-10-214-524-29

Query Match      79.4%; Score 77; DB 4; Length 577;
Best Local Similarity 77.8%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
      ||||| :||| :|
Db      295 VDGQKAENLFFYTAPPKR 312

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Job time : 90.9091 secs
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 9.27273 Seconds  
(without alignments)  
133.695 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97  
Sequence: 1 VDGQKATNIPYTPAGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*

- 1: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	44.3	254	6	US-10-471-571A-726
2	42	43.3	644	7	US-11-330-403-6482
3	42	43.3	644	7	US-11-330-403-15095
4	42	43.3	697	6	US-10-449-902-38427
5	42	43.3	985	7	US-11-342-171-6
6	42	43.3	985	7	US-11-342-171-66
7	41.5	42.8	582	7	US-11-330-403-14312
8	41.5	42.8	582	7	US-11-330-403-15230
9	40.5	41.8	582	7	US-11-330-403-15597
10	39	40.2	361	6	US-10-953-349-19539
11	39	40.2	361	7	US-11-056-355B-59400
12	39	40.2	371	6	US-10-953-349-5963
13	39	40.2	372	6	US-10-953-349-5962
14	39	40.2	374	6	US-10-953-349-5961
15	39	40.2	404	6	US-10-953-349-19538
16	39	40.2	404	7	US-11-056-355B-59399
17	39	40.2	408	6	US-10-953-349-19537
18	39	40.2	408	7	US-11-056-355B-59398
19	39	40.2	467	7	US-11-330-403-1235
20	39	40.2	505	7	US-11-330-403-1258
21	39	40.2	520	7	US-11-330-403-1582
22	39	40.2	520	7	US-11-330-403-11857
23	39	40.2	651	7	US-11-330-403-8900
24	38.5	39.7	394	6	US-10-471-571A-2218
25	38	39.2	55	7	US-11-056-355B-529

26	38	39.2	80	7	US-11-330-403-2450	Sequence 2450, Ap
27	38	39.2	113	6	US-10-471-571A-1112	Sequence 1112, Ap
28	38	39.2	133	7	US-11-056-355B-19386	Sequence 19386, A
29	38	39.2	171	6	US-10-471-571A-2022	Sequence 2022, Ap
30	38	39.2	239	7	US-11-330-403-3689	Sequence 3689, Ap
31	38	39.2	241	6	US-10-471-571A-728	Sequence 728, App
32	38	39.2	250	7	US-11-330-403-15600	Sequence 15600, A
33	38	39.2	287	7	US-11-330-403-13777	Sequence 13777, A
34	38	39.2	328	7	US-11-330-403-1378	Sequence 1378, Ap
35	38	39.2	417	7	US-11-056-355B-82642	Sequence 82642, A
36	38	39.2	502	6	US-10-565-233-14	Sequence 14, Appl
37	38	39.2	538	7	US-11-330-403-12046	Sequence 12046, A
38	38	39.2	579	7	US-11-330-403-2402	Sequence 2402, Ap
39	38	39.2	579	7	US-11-330-403-6386	Sequence 6386, Ap
40	38	39.2	579	7	US-11-330-403-11265	Sequence 11265, A
41	38	39.2	579	7	US-11-330-403-18232	Sequence 18232, A
42	38	39.2	581	7	US-11-330-403-1293	Sequence 1293, Ap
43	38	39.2	946	6	US-10-449-902-50315	Sequence 50315, A
44	38	39.2	1070	7	US-10-449-902-50315	Sequence 4839, A
45	38	39.2	1070	7	US-11-056-355B-46211	Sequence 46211, A

ALIGNMENTS

RESULT 1  
US-10-471-571A-726  
; Sequence 726, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026927W0  
; CURRENT APPLICATION NUMBER: US/10/471,571A  
; CURRENT FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: SeqWin99, version 1.03  
; SEQ ID NO 726  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(254)  
; OTHER INFORMATION: serine protease  
US-10-471-571A-726

Query Match 44.3%; Score 43; DB 6; Length 254;  
Best Local Similarity 88.9%; Pred. No. 8.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 5 KATNIPPYT 13  
Db 58 KDTNIPPYT 66

RESULT 2  
US-11-330-403-6482  
; Sequence 6482, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 6482  
; LENGTH: 644  
; TYPE: PRT  
; ORGANISM: Xanthomonas axonopodis pv. glycines



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: PatentIn Release #1.25  
APPLICATION NUMBER: US/11/342,171  
FILING DATE: 27-JAN-2006  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,190  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,597  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 39116-A  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 985 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-11-342-171-66

Query Match 43.3%; Score 42; DB 7; Length 985;  
Best Local Similarity 50.0%; Pred. No. 58;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIFPYTAPG 16  
| : : : : :  
DB 416 GSENTLFTTAPG 429

RESULT 7  
US-11-330-403-14312  
; Sequence 14312, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 14312  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Populus tomentosa  
US-11-330-403-14312

Query Match 42.8%; Score 41.5; DB 7; Length 582;  
Best Local Similarity 57.9%; Pred. No. 40;  
Matches 11; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 VDGQKATNIFPYTA---PG 16  
| | | | |  
DB 110 VDGSKATGAFILTASHNPG 128

RESULT 8  
US-11-330-403-15230  
; Sequence 15230, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B

; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 15230  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Populus tremula x Populus tremuloides  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(582)  
; OTHER INFORMATION: unsure at all xaa locations  
US-11-330-403-15230

Query Match 42.8%; Score 41.5; DB 7; Length 582;  
Best Local Similarity 57.9%; Pred. No. 40;  
Matches 11; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 VDGQKATNIFPYTA---PG 16  
| | | | |  
DB 110 VDGSKATGAFILTASHNPG 128

RESULT 9  
US-11-330-403-15597  
; Sequence 15597, Application US/11330403  
; Publication No. US20060159563A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53629)B  
; CURRENT APPLICATION NUMBER: US/11/330,403  
; CURRENT FILING DATE: 2006-01-12  
; NUMBER OF SEQ ID NOS: 19250  
; SEQ ID NO 15597  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Pisum sativum  
US-11-330-403-15597

Query Match 41.8%; Score 40.5; DB 7; Length 582;  
Best Local Similarity 57.9%; Pred. No. 60;  
Matches 11; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 VDGQKATNIFPYTA---PG 16  
| | | | |  
DB 110 VDGSKATGAFILTASHNPG 128

RESULT 10  
US-10-953-349-19539  
; Sequence 19539, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19539  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-19539

Query Match 40.2%; Score 39; DB 6; Length 361;  
Best Local Similarity 44.4%; Pred. No. 65;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPGKQ 18  
| | | | |

Db 124 VDGKKVKRKHPTTEKE 141

## RESULT 11

US-11-056-355B-59400  
; Sequence 59400, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 59400  
; LENGTH: 361  
; TYPE: prt  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(361)  
; OTHER INFORMATION: Ceres Seq. ID no. 14307779  
US-11-056-355B-59400

Query Match 40.2%; Score 39; DB 7; Length 361;  
Best Local Similarity 44.4%; Pred. No. 65;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAGKQ 18  
|||:| |||:  
Db 124 VDGKKVKRKHPTTEKE 141

## RESULT 12

US-10-953-349-5963  
; Sequence 5963, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5963  
; LENGTH: 371  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-5963

Query Match 40.2%; Score 39; DB 6; Length 371;  
Best Local Similarity 54.5%; Pred. No. 66;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYT 13  
|:| | |:  
Db 349 GEKIVNLIPYT 359

## RESULT 13

US-10-953-349-5962  
; Sequence 5962, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5962  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-5962

Query Match 40.2%; Score 39; DB 6; Length 404;  
Best Local Similarity 44.4%; Pred. No. 73;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAGKQ 18  
|||:| |||:  
Db 124 VDGKKVKRKHPTTEKE 141

; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5962  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-5962

Query Match 40.2%; Score 39; DB 6; Length 372;  
Best Local Similarity 54.5%; Pred. No. 67;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYT 13  
|:| | |:  
Db 350 GEKIVNLIPYT 360

## RESULT 14

US-10-953-349-5961  
; Sequence 5961, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5961  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-5961

Query Match 40.2%; Score 39; DB 6; Length 374;  
Best Local Similarity 54.5%; Pred. No. 67;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYT 13  
|:| | |:  
Db 352 GEKIVNLIPYT 362

## RESULT 15

US-10-953-349-19538  
; Sequence 19538, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19538  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-19538

Query Match 40.2%; Score 39; DB 6; Length 404;  
Best Local Similarity 44.4%; Pred. No. 73;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAGKQ 18  
|||:| |||:  
Db 124 VDGKKVKRKHPTTEKE 141



Db 167 VDGKKVRRKHPYTEKEKE 184

Search completed: August 30, 2006, 04:35:58  
Job time : 10.2727 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	49	51.0	616	2	E85508	hypothetical prote
2	49	51.0	616	2	E90657	hypothetical prote
3	47	49.0	721	2	JC7557	lipidoxin - mouse
4	46	47.9	262	2	AG3034	inositol monophosp
5	46	47.9	297	2	E98251	similar to mcb177
6	45	46.9	1536	1	RG3YS3	regulatory protein
7	43	44.8	105	2	T42322	hypothetical prote
8	43	44.8	284	2	G83358	probable ATP-bindi
9	43	44.8	654	2	H86717	hypothetical prote
10	42	43.8	185	2	D95115	thioredoxin family
11	42	43.8	191	2	H97984	conserved hypothet
12	42	43.8	218	2	S76407	phosphoribosylant
13	42	43.8	271	2	T21777	hypothetical prote
14	42	43.8	359	2	T06532	pyruvate dehydroge
15	42	43.8	359	2	S35157	Delta6 fatty acid
16	42	43.8	702	2	E69498	hypothetical prote
17	42	43.8	817	2	T16409	hypothetical prote
18	42	43.8	1744	2	A59370	teasin, cardiac mu
19	41	42.7	133	2	H72459	probable ribosomal
20	41	42.7	287	1	S76736	hypothetical prote
21	41	42.7	305	2	F86744	tagatose-6-phospha
22	41	42.7	419	2	G84503	hypothetical prote
23	41	42.7	477	2	T37791	probable rna polym
24	41	42.7	535	2	T07969	probable reticulim
25	41	42.7	630	2	T31798	hypothetical prote
26	41	42.7	1020	2	A96701	tetrathionate redu
27	41	42.7	1270	2	E96669	protein FIN19.11
28	41	42.7	2126	2	F70522	probable polyketid
29	40.5	42.2	2237	2	AB0372	phosphoribosylam

```

Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDEQFPQ--HGLVK 17
   ||:::|::|::|::|
Db 58 QKIEDFPQLTHGLIK 73

RESULT 3
JC7557
lipidosin - mouse
N;Alternate names: lipidosin-related protein
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7557
R;Moriya-Sato, A.; Hida, A.; Inagawa-Ogaishiwa, M.; Wada, M.R.; Sugiyama, K.; Shimizu, J.
Biochem. Biophys. Res. Commun. 279, 62-68, 2000
A;Title: Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.
A;Reference number: JC7557; MUID: 20563802; PMID:11112418
A;Contents: Brain
A;Accession: JC7557
A;Molecule type: mRNA
A;Residues: 1-721 <MOR>
A;Cross-references: UNIPROT:Q99PUS; UNIPARC:UPI000017A518
C;Comment: This protein possesses long-chain acyl-CoA synthetase activity and catalyzes
tion and the impairment of fatty acid metabolism in X-linked adrenoleukodystrophy. This
in human X-linked adrenoleukodystrophy.
C;Keywords: adrenoleukodystrophy

Query Match 49.0%; Score 47; DB 2; Length 721;
Best Local Similarity 53.3%; Pred. No. 8.9;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGL 15
   ||||: : : |||
Db 44 IDGQTLSKESFSHGL 58

RESULT 4
AG3034
inositol monophosphatase family protein [imported] - Agrobacterium tumefaciens (strain C
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG3034
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG3034
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <KUR>
A;Cross-references: UNIPROT:Q8U945; UNIPARC:UPI0000164892; GB:AE008689; PIDN:AAL44693.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3885
A;Map position: linear chromosome
C;Superfamily: suppressor protein subh

Query Match 47.9%; Score 46; DB 2; Length 262;
Best Local Similarity 54.5%; Pred. No. 4.2;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGLV 16
   ::|||::|::|
Db 59 IEERFPQHGL 69

RESULT 5

```

```

E98251
similar to mlcb1779.29 (probable monophosphatase gene) in mycobacterium leprae [imported]
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E98251
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman,
R;Goodner, B.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E98251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <KUR>
A;Cross-references: UNIPROT:Q8U945; UNIPARC:UPI00000D237F; GB:AE007870; PIDN:AAK89535.1;
C;Genetics:
A;Gene: AGR_L1926
A;Map position: linear chromosome
C;Superfamily: suppressor protein subh

Query Match 47.9%; Score 46; DB 2; Length 297;
Best Local Similarity 54.5%; Pred. No. 4.8;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGLV 16
   ::|||::|::|
Db 94 IEERFPQHGL 104

RESULT 6
RGBYS3
regulatory protein SIN3 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O2385; protein YOL004w
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: S66686; A36381; A41957; S12068; S22283
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S66686
A;Molecule type: DNA
A;Residues: 1-1536 <HUG>
A;Cross-references: UNIPROT:P22579; UNIPARC:UPI0000052F61; EMBL:274746; NID:gl149766; PI
A;Experimental source: strain S288C
R;Wang, H.; Clark, I.; Nicholson, P.R.; Herskowitz, I.; Stillman, D.J.
Mol. Cell. Biol. 10, 5927-5936, 1990
A;Title: The Saccharomyces cerevisiae SIN3 gene, a negative regulator of HO, contains fo
A;Reference number: A36381; MUID:91042523; PMID:2233725
A;Accession: A36381
A;Molecule type: DNA
A;Residues: 1-510,'AO',511-1536 <WAN>
A;Cross-references: UNIPARC:UPI0000168D4F; GB:M36822; NID:gl72093; PIDN:AAA34839.1; PID:
R;Vidal, M.; Strich, R.; Esposito, R.E.; Gaber, R.F.
Mol. Cell. Biol. 11, 6306-6316, 1991
A;Title: RPD1 (SIN3/UME4) is required for maximal activation and repression of diverse y
A;Reference number: A41957; MUID:92049361; PMID:1944290
A;Accession: A41957
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 227-285;414-441,'DE',444-472;667-725;1140-1200 <VID>
A;Cross-references: UNIPARC:UPI0000174911; UNIPARC:UPI0000174912; UNIPARC:UPI0000174913;
C;Genetics:
A;Gene: SGD.SIN3; SD11; UME4; RPD1; MIPS.YOL004w
A;Cross-references: SGD:S0005364; MIPS.YOL004w
A;Map position: 15L
C;Superfamily: regulatory protein SIN3
C;Keywords: nucleus; transcription regulation
F;480-519/Region: glutamine-rich

Query Match 46.9%; Score 45; DB 1; Length 1536;
Best Local Similarity 53.3%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 IDGQKVDQPPQHG 15  
|||:|||||:  
Db 1370 IDGTEVDEEFSPEGI 1384

RESULT 7  
T42322  
hypothetical protein - phase SPP1  
C/Species: phase SPP1  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T42322  
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.  
Gene 204, 201-212, 1997  
A/Title: The complete nucleotide sequence and functional organization of Bacillus subtilis  
A/Reference number: Z22137; MUID:98094274; PMID:9434185  
A/Accession: T42322  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-105 <ALO>  
A/Cross-references: UNIPROT:O48482; UNIPARC:UPI0000009B161; EMBL:X97918; PIDN:CAA66529.1

Query Match 44.8%; Score 43; DB 2; Length 105;  
Best Local Similarity 50.0%; Pred. No. 4.9;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IDGQKVDQPPQHG 18  
|||:|||||:  
Db 5 INQKIGEWIERGRVDQ 22

RESULT 8  
G83358  
probable ATP-binding component of ABC transporter PA2294 [imported] - Pseudomonas aeruginosa  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: G83358  
R;Stover, C.K.; Fiam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.B.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: G83358  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-284 <STO>  
A/Cross-references: UNIPROT:Q91111; UNIPARC:UPI000000C5650; GB:AE004655; GB:AE004091; NID  
A/Experimental source: strain PA01  
C/Genetics:  
A/Gene: PA2294

Query Match 44.8%; Score 43; DB 2; Length 284;  
Best Local Similarity 44.4%; Pred. No. 15;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 IDGQKVDQPPQHG 18  
|||:|||||:  
Db 73 VDGRSVEGSPQGMVQ 90

RESULT 9  
H86717  
hypothetical protein ynfB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C/Species: Lactococcus lactis subsp. lactis  
C/Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: H86717  
R;Bolotin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, G.  
Genome Res. 11, 731-753, 2001  
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss  
A/Reference number: A86625; MUID:21235186; PMID:11337471  
A/Accession: H86717  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-654 <STO>  
A/Cross-references: UNIPROT:Q9CH17; UNIPARC:UPI000000C68D4; GB:AE005176; PID:gi2723660; P  
A/Experimental source: strain IL1403  
C/Genetics:  
A/Gene: ynfB

Query Match 44.8%; Score 43; DB 2; Length 654;  
Best Local Similarity 43.8%; Pred. No. 39;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 IDGQKVDQPPQHG 16  
|||:|||||:  
Db 441 IDHRRDDDFPERALL 456

RESULT 10  
D95115  
thioredoxin family protein [imported] - Streptococcus pneumoniae (strain TIGR4)  
C/Species: Streptococcus pneumoniae  
C/Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C/Accession: D95115  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A/Reference number: A95000; MUID:21357209; PMID:11463916  
A/Accession: D95115  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-185 <KUR>  
A/Cross-references: UNIPROT:Q97R36; UNIPARC:UPI0000051693; GB:AE005672; PIDN:AAK75117.1;  
A/Experimental source: strain TIGR4  
C/Genetics:  
A/Gene: SP1000

Query Match 43.8%; Score 42; DB 2; Length 185;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQPPQ 12  
|||:|||||:  
Db 112 IQGEKTVEQPPQ 123

RESULT 11  
H97984  
conserved hypothetical protein spr0904 [imported] - Streptococcus pneumoniae (strain R6)  
C/Species: Streptococcus pneumoniae  
C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C/Accession: H97984  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A/Reference number: A97872; MUID:21429245; PMID:11544234  
A/Accession: H97984  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-191 <KUR>  
A/Cross-references: UNIPROT:Q8DQ10; UNIPARC:UPI000000E3552; GB:AE007317; PIDN:AAK99708.1;  
C/Genetics:  
A/Gene: spr0904

Query Match 43.8%; Score 42; DB 2; Length 191;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQPPQ 12  
|||:|||||:



RESULT 2  
Q8VOF9\_XENBV PRELIMINARY; PRT; 1089 AA.  
AC Q8VOF9;  
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2002, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE Peptide synthetase XpsA.  
GN Name:xpsA;  
OS Xenorhabdus bovienii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria;  
OC Enterobacteriaceae; Xenorhabdus.  
OX NCBI TaxID=40576;

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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=T228;
RA Pinyon R.A., Thomas C.J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF455810; AAL57599.1; -; Genomic_DNA.
DR HSP; P14687; IAMU.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA adenyl_dom.
DR InterPro; IPR009081; ACP-like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR006163; Phosphopanteth_bd.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00668; Condensation; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRfams; TIGR01733; AA-adenyl-dom; 1.
DR PROSITE; PS50075; ACP DOMAIN; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 1089 AA; 122987 MW; FF42C1A12506CBF9 CRC64;

Query Match 53.1%; Score 51; DB 2; Length 1089;
Best Local Similarity 53.9%; Pred. No. 40;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DGQKVDQFPQHGVLVKQ 18
Db 470 DFNKTKRPFQHALHQ 486

RESULT 3
ID Q5GR68_ALCXX PRELIMINARY; PRT; 1008 AA.
AC Q5GR68;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Transposase.
GN Name=tnpA;
OS Alkaligenes xylosoxydans (Achromobacter xylosoxydans).
OG Plasmid pA81.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alkaligenaceae; Achromobacter.
OX NCBI_TaxID=85698;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=A8;
RA Jencova V., Strnad H., Chodora Z., Ulbrich P., Hickey W.J., Paces V.;
RT "Chlorocatechol catabolic enzymes from Achromobacter xylosoxydans
RT A8.";
RL Int. Biodeterior. Biodegradation 54:175-181 (2004).
[2]
RC NUCLEOTIDE SEQUENCE.
RA Jencova V.;
RC STRAIN=A8;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC -----
DR EMBL; AJ515144; CA147903.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR002513; Transposase_7.
DR Pfam; PF01526; Transposase_7; 1.

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KW Plasmid.
SQ SEQUENCE 1008 AA; 114817 MW; A9F92682878061E5 CRC64;

Query Match 52.6%; Score 50.5; DB 2; Length 1008;
Best Local Similarity 45.5%; Pred. No. 45;
Matches 10; Conservative 3; Mismatches 0; Indels 9; Gaps 1;

Qy 1 IDG-----OKVDEQFPQH 13
Db 516 VDGLKQLLTETAEKVDEEFPQH 537

RESULT 4
Q45W0_9BURK
ID Q45W0_9BURK PRELIMINARY; PRT; 271 AA.
AC Q45W0;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE ABC transporter.
GN ORFNames=BcNDRAFT_2623;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAH10100019; EAM11227.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019866; C:organelle inner membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_Arpase.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR02110; ANK.
DR Pfam; PF00005; ABC_tran; 1.
DR PRINTS; PR01415; ANKYRIN.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
SQ SEQUENCE 271 AA; 29686 MW; E3976DF676E02527 CRC64;

Query Match 52.1%; Score 50; DB 2; Length 271;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVKQ 18
Db 470 DFNKTKRPFQHALHQ 486

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Db      85 VDGERVDRPHDRGLVFQ 102

RESULT 5
Q4LMX1_9BURK
ID      Q4LMX1_9BURK      PRELIMINARY;      PRT;      271 AA.
AC      Q4LMX1_
DT      02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT      02-AUG-2005, sequence version 1.
DT      21-FEB-2006, entry version 7.
DE      ABC transporter.
GN      ORFNames=Bcen2424DRAFT_2386;
OS      Burkholderia cenocepacia H12424.
OC      Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC      Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX      NCBI_TaxID=331272;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=H12424;
RG      US DOE Joint Genome Institute (JGI-RGF);
RA      Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA      Hammon N., Israni S., Pitluck S., Richardson P.;
RT      "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT      H12424."
RL      Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=H12424;
RG      US DOE Joint Genome Institute (JGI-ORNL);
RA      Larimer F., Land M.;
RT      "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT      H12424."
RL      Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC      -1- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; AAHL01000041; EAM17437.1; -; Genomic_DNA.
CC      GO; GO:0016020; C:membrane; IEA.
CC      GO; GO:0019866; C:organelle inner membrane; IEA.
CC      GO; GO:0005524; F:ATP binding; IEA.
CC      GO; GO:0016987; F:ATPase activity; IEA.
CC      GO; GO:0000166; F:nucleotide binding; IEA.
CC      GO; GO:0006810; P:transport; IEA.
CC      InterPro; IPR003593; AAA_ATPase.
CC      InterPro; IPR003439; ABC_transp_like.
CC      Pfam; PF00005; ABC_tran; 1.
CC      PRINTS; PR01415; ANKYRIN.
CC      ProDom; PD000006; ABC transporter; 1.
CC      SMART; SM00382; AAA_1.
CC      PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
CC      PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
SQ      SEQUENCE 271 AA; 29686 MW; E9976DF676E02527 CRC64;

Query Match 52.1%; Score 50; DB 2; Length 271;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGLVKQ 18
      :||:|||||
Db      85 VDGERVDRPHDRGLVFQ 102

RESULT 6
Q88RC3_PSEPK
ID      Q88RC3_PSEPK      PRELIMINARY;      PRT;      283 AA.
AC      Q88RC3;
DT      01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT      01-JUN-2003, sequence version 1.

Query Match 52.1%; Score 50; DB 2; Length 271;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGLVKQ 18
      :||:|||||
Db      85 VDGERVDRPHDRGLVFQ 102

RESULT 6
Q88RC3_PSEPK
ID      Q88RC3_PSEPK      PRELIMINARY;      PRT;      283 AA.
AC      Q88RC3;
DT      01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT      01-JUN-2003, sequence version 1.
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DT      21-FEB-2006, entry version 23.
DE      Nitrate ABC transporter, ATP-binding protein, putative.
GN      OrderedLocusNames=PP0209; ORFNames=PP_0209;
OS      Pseudomonas putida (strain KT2440).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC      Pseudomonadaceae; Pseudomonas.
OX      NCBI_TaxID=160488;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      MEDLINE=22423060; PubMed=12534463;
RC      DOI=10.1046/j.1462-2920.2002.00366.x;
RA      Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA      Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA      Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA      Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA      Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA      Moazzes A., Utterback T.R., Rizzo M., Lee K., Kosack D., Meestl D.,
RA      Wedler H., Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,
RA      Kiewitz C., Eisen J.A., Timmis K.N., Duisterhoef A., Tummeler B.,
RA      Fraser C.M.;
RT      "Complete genome sequence and comparative analysis of the
RT      metabolically versatile Pseudomonas putida KT2440."
RL      Environ. Microbiol. 4:799-808(2002).
CC      -1- SIMILARITY: Belongs to the ABC transporter family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; AE015451; AAN65842.1; -; Genomic_DNA.
CC      HSSP; Q9YGA6; 1G29.
CC      TIGR; PP0209; -.
CC      GO; GO:0016020; C:membrane; IEA.
CC      GO; GO:0005524; F:ATP binding; IEA.
CC      GO; GO:0016987; F:ATPase activity; IEA.
CC      GO; GO:0000166; F:nucleotide binding; IEA.
CC      GO; GO:0006810; P:transport; IEA.
CC      InterPro; IPR003593; AAA_ATPase.
CC      InterPro; IPR003439; ABC_transp_like.
CC      Pfam; PF00005; ABC_tran; 1.
CC      ProDom; PD000006; ABC transporter; 1.
CC      SMART; SM00382; AAA_1.
CC      PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
CC      PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW      ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ      SEQUENCE 283 AA; 31651 MW; DA1B21FCA2223A4A CRC64;

Query Match 52.1%; Score 50; DB 2; Length 283;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGLVKQ 18
      :||:|||||
Db      73 VDCQVDPSPQGMVFQ 90

RESULT 7
Q3AG05_CARHZ
ID      Q3AG05_CARHZ      PRELIMINARY;      PRT;      370 AA.
AC      Q3AG05;
DT      22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT      22-NOV-2005, sequence version 1.
DT      07-FEB-2006, entry version 4.
DE      Putative serine protease Do.
GN      OrderedLocusNames=CHY_0057;
OS      Carboxydotherrus hydrogenoformans (strain Z-2901 / DSM 6008).
OC      Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae;
OC      Carboxydotherrus.
OX      NCBI_TaxID=246194;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
RX      PubMed=16311624; DOI=10.1371/journal.pgen.0010065;
RA      Wu M., Ren Q., Durkin A.S., Daugherty S.C., Brinkac L.M., Dodson R.J.,
RA      Madupu R., Sullivan S.A., Kolonay J.F., Nelson W.C., Taiton L.J.,
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RA Jones K.M., Ulrich L.E., Gonzalez J.M., Zhulin I.B., Robb F.T.,
RA Eisen J.A.;
RT "Life in hot carbon monoxide: the complete genome sequence of
RT Carboxydotherrmus hydrogenoformans Z-2901.";
RL PLOS Genet. 1:563-574(2005).
CC -1- SIMILARITY: Contains 1 PDZ (DHR) domain.
CC -----
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CC -----
DR EMBL; CP000141; ABB15592.1; -; Genomic_DNA.
DR TIGR; CHY 0057; -.
DR GO; GO:0076021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
KW Complete proteome; Hydrolase; Membrane; Protease; Serine protease;
KW Transmembrane.
SQ SEQUENCE 370 AA; 39702 MW; B512C002579F1384 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 370;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDEQFPQHGLVK 18
Db 277 IEQQTIDEFPAQYKGLK 294

RESULT 8
Q325C8 SHISS
ID Q325C8 SHISS PRELIMINARY; PRT; 616 AA.
AC Q325C8 SHISS
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN OrderedLocusNames=SSO_0250; ORFNames=SSO_0250;
OS Shigella sonnei (strain Ss046).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300269;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki1954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).
CC -----
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CC -----
DR EMBL; CP000038; AAZ87034.1; -; Genomic_DNA.
DR InterPro; IPR010272; DUF879_bac.
DR Pfam; PF05947; DUF879; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 616 AA; 71178 MW; 1C4B9A3B0CE75306 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 616;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDEQFPQ--HGLVK 17
Db 58 QKIEDEFPETHGLIK 73

RESULT 9
Q8X7U6_ECO57
ID Q8X7U6_ECO57 PRELIMINARY; PRT; 616 AA.
AC Q8X7U6; Q7AHU17;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE No significant matches (Hypothetical protein ECS0229).
GN OrderedLocusNames=ECS0229, 20260;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=11206551; PubMed=11258796; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Rose D.J., Mayhew G.F., Burland V., Mau B., Glasner J.D.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RMD 050952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -----
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CC -----
DR EMBL; AE005174; AAG54529.1; -; Genomic_DNA.
DR EMBL; BA000007; BAB33652.1; -; Genomic_DNA.
DR PIR; E85508; E85508.
DR PIR; E90657; E90657.
DR BioCyc; ECOL83334-1:ECS0229-MONOMER; -.
DR InterPro; IPR010272; DUF879_bac.
DR Pfam; PF05947; DUF879; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 616 AA; 71186 MW; 1FBC0A5128341E30 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 616;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDEQFPQ--HGLVK 17
Db 58 QKIEDEFPETHGLIK 73

RESULT 10
Q61Y77_CAEBR
ID Q61Y77_CAEBR PRELIMINARY; PRT; 345 AA.
AC Q61Y77;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein CBG03674.
GN Name=CBG03674;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blaslar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuwabara P.B., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Schumann M.,
RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of Caenorhabditis briggsae: a platform for
RT comparative genomics";
RL PLoS Biol. 1:166-192(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; CAAC01000016; CAE60129.1; -; Genomic DNA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 2.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 345 AA; 38450 MW; 744C79ED3D80408D CRC64;

Query Match 50.0%; Score 48; DB 2; Length 345;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDGQKVDEQFPQHG 14
Db 80 VSGKRVDEQFVQHG 93

RESULT 11
Q43G89 9CHLB PRELIMINARY; PRT; 442 AA.
AC Q43G89;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE Similar to Uncharacterized protein conserved in bacteria.
GN ORFNames=Cpha266DRAFT_1504;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Felodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAI01000015; EAM34597.1; -; Genomic DNA.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF05990; IGF900; 1.
DR PROSITE; PS00230; I9_MHC; UNKNOWN_1.
SQ SEQUENCE 442 AA; 48627 MW; 4877E0BFF60B46FC CRC64;

Query Match 50.0%; Score 48; DB 2; Length 442;
Best Local Similarity 64.3%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 IDGQKVDEQFPQHG 14
Db 390 IDASKVDNGFPFGH 403

RESULT 12
Q2JEG1 9ACTO PRELIMINARY; PRT; 851 AA.
AC Q2JEG1;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DE PHA domain containing protein.
DE ORFNames=Francis3_0947;
GN Frankia sp. Cc13.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Frankineae; Frankiaceae; Frankia.
OX NCBI_TaxID=106370;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Cc13;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Goltzman E., Martinez M.,
RA Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A., Francino P.,
RA Benson D.R., Huang Y., Mastrorunzio J., Bickhart D., Niemann J.,
RA Rawnsley T., Tisa L.S., Richardson P.;
RT "Complete sequence of Frankia sp. Cc13.";
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000249; ABD1031.1; -; Genomic DNA.
SQ SEQUENCE 851 AA; 92384 MW; B4197D33CA0FD261 CRC64;

Query Match 50.0%; Score 48; DB 2; Length 851;
Best Local Similarity 52.9%; Pred. No. 97;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 IDGQKVDEQFPQHG 17
Db 66 IDGQRMPEIVPVHGEVR 82

RESULT 13
Q47YD9 COLP3 PRELIMINARY; PRT; 421 AA.
AC Q47YD9;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE Efflux transporter, RND family, MFP subunit subfamily.
GN OrderedLocusNames=CPS_3507;
OS Colwellia psychrerythraea (strain 34H / ATCC BAA-681) (Vibrio
OS psychrerythrus).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

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RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptomic landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard R., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelain A., Schneider C., Sempke C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).

RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [9]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
 RX STRAIN=C57BL/6J; TISSUE=Brain;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sodabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Query Match 49.0%; Score 47; DB 2; Length 721;  
 Best Local Similarity 53.3%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 IDGQKVDQEPQHQGL 15  
 ||||| : : : |||||  
 Db 44 IDGQTLKSPSHGL 58

Search completed: August 30, 2006, 04:29:09

Job time : 74.1818 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 17.8182 Seconds  
(without alignments)  
88.424 Million cell updates/sec

Title: US-10-758-165a-11

Perfect score: 96  
Sequence: 1 IDGQKVDQF--POHGLVKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	47.9	195	2	US-09-248-796A-19566
2	45	46.9	1512	2	US-09-328-352-5163
3	45	46.9	1536	2	US-09-487-558B-322
4	43	44.8	612	2	US-09-252-991A-25727
5	42	43.8	137	2	US-08-961-083-40
6	42	43.8	137	2	US-09-536-784-40
7	42	43.8	137	2	US-09-785-271-40
8	42	43.8	137	2	US-09-765-272A-40
9	42	43.8	185	2	US-09-583-110-5222
10	42	43.8	194	2	US-09-107-433-5104
11	42	43.8	228	2	US-09-134-000C-6247
12	42	43.8	359	1	US-08-307-382-2
13	42	43.8	359	1	US-08-366-779-2
14	42	43.8	359	1	US-08-478-727-2
15	42	43.8	359	1	US-08-473-508-2
16	42	43.8	359	1	US-08-789-936-2
17	42	43.8	359	1	US-08-833-610-6
18	42	43.8	359	2	US-08-834-033A-16
19	42	43.8	359	2	US-08-934-254-2
20	42	43.8	359	2	US-09-377-452-6
21	42	43.8	359	2	US-09-685-775-2
22	42	43.8	363	2	US-09-108-020-44
23	42	43.8	363	2	US-09-685-296-44
24	42	43.8	590	2	US-09-489-039A-8178
25	41	42.7	297	2	US-09-248-796A-25364
26	41	42.7	381	2	US-09-248-796A-17552

27	41	42.7	394	2	US-09-252-991A-32539	Sequence 32539, A
28	41	42.7	535	2	US-09-589-733C-18	Sequence 18, Appl
29	41	42.7	536	2	US-09-258-031C-77	Sequence 77, Appl
30	40.5	42.2	246	2	US-09-543-681A-8212	Sequence 8212, Ap
31	40	41.7	230	2	US-09-252-991A-25914	Sequence 25914, A
32	40	41.7	344	2	US-09-252-991A-30083	Sequence 30083, A
33	40	41.7	666	2	US-09-270-767-46736	Sequence 46736, A
34	39.5	41.1	79	2	US-09-248-796A-23915	Sequence 23915, A
35	39.5	41.1	912	1	US-08-951-871-2	Sequence 2, Appli
36	39	40.6	195	2	US-09-252-991A-21451	Sequence 21451, A
37	39	40.6	271	1	US-08-152-019A-28	Sequence 28, Appl
38	39	40.6	336	1	US-07-667-276A-8	Sequence 8, Appli
39	39	40.6	411	2	US-09-134-000C-3961	Sequence 3961, Ap
40	39	40.6	416	2	US-09-134-000C-6248	Sequence 6248, Ap
41	39	40.6	463	2	US-09-198-452A-115	Sequence 115, App
42	39	40.6	468	2	US-09-438-185A-100	Sequence 100, App
43	39	40.6	505	2	US-09-252-991A-29343	Sequence 29343, A
44	39	40.6	510	2	US-09-270-767-46399	Sequence 46399, A
45	39	40.6	1725	2	US-09-562-702A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-09-248-796A-19566  
; Sequence 19566, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19566  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19566

Query Match 47.9% Score 46; DB 2; Length 195;  
Best Local Similarity 55.0%; Pred. No. 4.5;  
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 IDGQKVDQF--POHGLVKQ 18  
:|||||:|  
Db 34 MDGQKVDVLLPPQHEIKKQ 53

RESULT 2  
US-09-328-352-5163  
; Sequence 5163, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5163  
; LENGTH: 1512  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5163

Query Match 46.9%; Score 45; DB 2; Length 1512;  
Best Local Similarity 50.0%; Pred. No. 70;  
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GQKVDEQFPQHGLVKQ 18  
Db 328 GDRDPLMPHGLVSVQ 343

RESULT 3  
US-09-487-558B-322  
; Sequence 322, Application US/09487558B  
; Patent No. 6949356  
; GENERAL INFORMATION:  
; APPLICANT: Busby, Robert  
; APPLICANT: Cali, Brian  
; APPLICANT: Hecht, Peter  
; APPLICANT: Holtzman, Doug  
; APPLICANT: Madden, Kevin  
; APPLICANT: Maxon, Mary  
; APPLICANT: Milne, Todd  
; APPLICANT: Royer, John  
; APPLICANT: Salama, Sofie  
; APPLICANT: Sherman, Amir  
; APPLICANT: Silva, Jeff  
; APPLICANT: Summers, Eric  
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
; FILE REFERENCE: 109272.130  
; CURRENT APPLICATION NUMBER: US/09/487.558B  
; CURRENT FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: US 60/487,558  
; PRIOR FILING DATE: 1999-10-20  
; NUMBER OF SEQ ID NOS: 446  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 322  
; LENGTH: 1536  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-487-558B-322

Query Match 46.9%; Score 45; DB 2; Length 1536;  
Best Local Similarity 53.3%; Pred. No. 71;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGL 15  
Db 1370 IDGTEVDEFSPEGI 1384

RESULT 4  
US-09-252-991A-25727  
; Sequence 25727, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 25727  
; LENGTH: 612  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-25727

Query Match 44.8%; Score 43; DB 2; Length 612;

Best Local Similarity 44.4%; Pred. No. 55;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGLVKQ 18  
Db 401 VDGRSVEGSPQRGMVFQ 418

RESULT 5  
US-08-961-083-40  
; Sequence 40, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION NUMBER: US/08/961,083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 137 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-961-083-40

Query Match 43.8%; Score 42; DB 2; Length 137;  
Best Local Similarity 66.7%; Pred. No. 15;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQ 12  
Db 93 IQGEKTEQFPQ 104

RESULT 6  
US-09-536-784-40  
; Sequence 40, Application US/09536784  
; Patent No. 6573082  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland



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;
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-536-784-40

Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQ 12
Db 93 IQEKTVEQFPQ 104

RESULT 7
US-09-765-271-40
; Sequence 40, Application US/09765271
; Patent No. 6887663
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,271
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/536,784
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-271-40

Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQ 12
Db 93 IQEKTVEQFPQ 104

RESULT 8
US-09-765-272A-40
; Sequence 40, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 454
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: Dell Latitude C610
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272A
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin J. Hymel
; REGISTRATION NUMBER: 45,414
; REFERENCE/DOCKET NUMBER: PB340P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-272A-40

Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQ 12
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Db 93 IQGKTVQPPQ 104

RESULT 9

US-09-583-110-5222

Sequence 5222, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

FILE REFERENCE: PATH00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 5222

LENGTH: 185

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-583-110-5222

Query Match 43.8%; Score 42; DB 2; Length 185;

Best Local Similarity 66.7%; Pred. No. 21;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQPPQ 12

Db 112 IQGKTVQPPQ 123

RESULT 10

US-09-107-433-5104

Sequence 5104, Application US/09107433

Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneka

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 5104:

SEQUENCE CHARACTERISTICS:

LENGTH: 194 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...194

SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

US-09-107-433-5104

Query Match 43.8%; Score 42; DB 2; Length 194;

Best Local Similarity 66.7%; Pred. No. 22;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQPPQ 12

Db 121 IQGKTVQPPQ 132

RESULT 11

US-09-134-000C-6247

Sequence 6247, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6247

LENGTH: 228

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-6247

Query Match 43.8%; Score 42; DB 2; Length 228;

Best Local Similarity 87.5%; Pred. No. 26;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FPQHGLVK 17

Db 174 FPQHGLLK 181

RESULT 12

US-08-307-382-2

Sequence 2, Application US/08307382

Patent No. 5552306

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

APPLICANT: Reddy, Avutu S.

APPLICANT: Nuccio, Michael

APPLICANT: Freyssinet, Georges L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC

TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,382
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/817,919
; FILING DATE: 08-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 8383Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-382-2

Query Match 43.8%; Score 42; DB 1; Length 359;
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 QKVDEQFPQHGLVKQ 18
Db 21 QRVDAYFAEHLTQR 35

RESULT 14
US-08-478-727-2
; Sequence 2, Application US/08478727
; Patent No. 5663068
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
; ACID BY A DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,727
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,382
; FILING DATE: 14-SEP-1994
; APPLICATION NUMBER: US 07/817,919
; FILING DATE: 08-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 8383Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-727-2

Query Match 43.8%; Score 42; DB 1; Length 359;
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 QKVDEQFPQHGLVKQ 18
Db 21 QRVDAYFAEHLTQR 35

RESULT 13
US-08-366-779-2
; Sequence 2, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,779
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
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Search completed: August 30, 2006, 04:33:00  
Job time : 18.8182 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 90.9091 Seconds  
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Title: US-10-758-165a-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQPPQGLVKQ 18

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Searched: 2097797 seqs, 463214958 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US09\_PUBCOMB.pcp.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	5	US-10-758-165-11
2	96	100.0	424	4	US-10-451-078-2
3	96	100.0	424	4	US-10-451-078-4
4	78	81.2	15	4	US-10-052-788-5
5	63	65.6	569	4	US-10-214-524-30
6	45	46.9	178	4	US-10-424-599-146307
7	45	46.9	504	4	US-10-282-122A-55836
8	45	46.9	685	6	US-11-037-143-19596
9	45	46.9	1536	3	US-09-801-368-322
10	44	45.8	89	4	US-10-424-599-205669
11	44	45.8	128	5	US-10-450-763-36065
12	44	45.8	130	4	US-10-424-599-145103
13	44	45.8	159	5	US-10-450-763-36064
14	44	45.8	387	4	US-10-437-963-154933
15	44	45.8	421	4	US-10-238-075-1472
16	43.5	45.3	718	4	US-10-017-161-784
17	43	44.8	70	6	US-11-188-298-3776
18	43	44.8	121	4	US-10-425-115-187877
19	43	44.8	146	4	US-10-425-114-46519
20	43	44.8	149	4	US-10-425-115-210792
21	43	44.8	152	4	US-10-425-114-42340
22	43	44.8	316	5	US-10-922-282-12
23	43	44.8	325	4	US-10-425-114-37611
24	43	44.8	346	4	US-10-425-114-39926
25	43	44.8	356	5	US-10-922-282-30
26	43	44.8	366	4	US-10-425-114-37769
27	43	44.8	371	4	US-10-425-114-48824

28	43	44.8	374	4	US-10-767-701-45372	Sequence 45372, A
29	43	44.8	374	4	US-10-425-115-216179	Sequence 216179, A
30	43	44.8	374	4	US-10-425-115-216182	Sequence 216182, A
31	43	44.8	375	4	US-10-767-701-42582	Sequence 42582, A
32	43	44.8	398	4	US-10-425-115-300080	Sequence 300080, A
33	43	44.8	403	4	US-10-425-114-40459	Sequence 40459, A
34	43	44.8	403	4	US-10-425-114-57233	Sequence 57233, A
35	43	44.8	409	4	US-10-425-114-46619	Sequence 46619, A
36	43	44.8	434	4	US-10-437-963-169342	Sequence 169342, A
37	43	44.8	605	4	US-10-424-599-157014	Sequence 157014, A
38	42	43.8	84	4	US-09-765-272-40	Sequence 40, Appl
39	42	43.8	137	3	US-11-106-649-40	Sequence 40, Appl
40	42	43.8	137	6	US-10-472-928-1980	Sequence 1980, Ap
41	42	43.8	185	5	US-10-474-776-661	Sequence 661, App
42	42	43.8	191	4	US-10-617-320-5104	Sequence 5104, Ap
43	42	43.8	194	5	US-10-282-122A-46126	Sequence 46126, A
44	42	43.8	199	4	US-10-369-493-2768	Sequence 2768, Ap
45	42	43.8	218	4		

ALIGNMENTS

RESULT 1

US-10-758-165-11  
; Sequence 11, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10758,165  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Equus caballus  
US-10-758-165-11

Query Match 100.0%; Score 96; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDQPPQGLVKQ 18  
Db 1 IDGQKVDQPPQGLVKQ 18

RESULT 2

US-10-451-078-2  
; Sequence 2, Application US/10451078  
; Publication No. US20040115764A1  
; GENERAL INFORMATION:  
; APPLICANT: Leibold, Wolfgang  
; APPLICANT: Bettina, Wagner  
; APPLICANT: Radbruch, Andreas  
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the Heavy Chain of an Equine IgE Allotype, Recombinant Immunoglobulins Obtained Using Them, and Corresponding Isotype-specific Monoclonal Antibodies and their Use  
; FILE REFERENCE: 03100177aa  
; CURRENT APPLICATION NUMBER: US/10/451,078  
; CURRENT FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: PCT/DE01/04810  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: DE 100 64 415.5  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.2

SEQ ID NO 2  
LENGTH: 424  
TYPE: PRT  
ORGANISM: Equus caballus  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (1)..(97)  
OTHER INFORMATION: CH1 domain, IgE allotype a  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (98)..(205)  
OTHER INFORMATION: CH2 domain, IgE allotype a  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (206)..(312)  
OTHER INFORMATION: CH3 domain, IgE allotype a  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (313)..(424)  
OTHER INFORMATION: CH4 domain, IgE allotype a  
US-10-451-078-2

Query Match 100.0%; Score 96; DB 4; Length 424;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDEQFPQHGLVKQ 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 145 IDGQKVDEQFPQHGLVKQ 162

RESULT 3  
US-10-451-078-4  
Sequence 4, Application US/10451078  
Publication No. US20040115764A1  
GENERAL INFORMATION:  
APPLICANT: Leibold, Wolfgang  
APPLICANT: Bettina, Wagner  
APPLICANT: Radbruch, Andreas  
TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the Heavy Chain of an Equine IgE Allotype, Recombinant  
TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding  
TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use  
FILE REFERENCE: 03100177aa  
CURRENT APPLICATION NUMBER: US/10/451.078  
CURRENT FILING DATE: 2003-12-24  
PRIOR FILING DATE: 2003-12-24  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: DE 100 64 415.5  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 4  
LENGTH: 424  
TYPE: PRT  
ORGANISM: Equus caballus  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (1)..(97)  
OTHER INFORMATION: CH1 domain, IgE allotype b  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (98)..(205)  
OTHER INFORMATION: CH2 domain, IgE allotype b  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (206)..(312)  
OTHER INFORMATION: CH3 domain, IgE allotype b  
FEATURE:  
NAME/KEY: Domain  
LOCATION: (313)..(424)  
OTHER INFORMATION: CH4 domain, IgE allotype b  
US-10-451-078-4

Query Match 100.0%; Score 96; DB 4; Length 424;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDEQFPQHGLVKQ 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 145 IDGQKVDEQFPQHGLVKQ 162

RESULT 4  
US-10-052-788-5  
Sequence 5, Application US/10052788  
Publication No. US20030087314A1  
GENERAL INFORMATION:  
APPLICANT: Gerishwin, Laurel J.  
APPLICANT: Pettigrew, Howard David  
APPLICANT: Kalina, Warren V.  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for Induction of Anti-IgE Antibodies  
FILE REFERENCE: 023070-121000US  
CURRENT APPLICATION NUMBER: US/10/052.788  
CURRENT FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: epitope peptide  
OTHER INFORMATION: P5, middle portion of C2 of equine IgE epsilon  
OTHER INFORMATION: heavy chain  
US-10-052-788-5

Query Match 81.2%; Score 78; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDEQFPQHGLVKQ 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 IDGQKVDEQFPQHGLVKQ 15

RESULT 5  
US-10-214-524-30  
Sequence 30, Application US/10214524  
Publication No. US20030073142A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Sway-Shen Alex  
APPLICANT: Yang, Yong-Min  
APPLICANT: Barankiewicz, Theresa J.  
APPLICANT: Chen, Zhong  
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
FILE REFERENCE: ICE-00101.P.1-1  
CURRENT APPLICATION NUMBER: US/10/214.524  
CURRENT FILING DATE: 2002-08-08  
PRIOR APPLICATION NUMBER: 60/312,120  
PRIOR FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 30  
LENGTH: 569  
TYPE: PRT  
ORGANISM: Horse (Equus caballus)  
US-10-214-524-30

Query Match 65.6%; Score 63; DB 4; Length 569;  
Best Local Similarity 66.7%; Pred. No. 0.13;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDEQFPQHGLVKQ 18

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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55836
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-55836

Query Match          46.9%; Score 45; DB 4; Length 504;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  IDGQKVDQEPQHGHL 15
        |||:|:|:|:|:|
Db      315  IDGERVDIQKPAHAI 329

RESULT 8
US-11-097-143-19596
; Sequence 19596, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19596
; LENGTH: 685
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-19596

Query Match          46.9%; Score 45; DB 6; Length 685;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3  GQKVDQEPQHGHLV 17
        |||:|:|:|:|
Db      577  GQGSNSYPEHGLV 591

RESULT 9
US-09-801-368-322
; Sequence 322, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:

```

APPLICANT: Busby, Robert  
APPLICANT: Cali, Brian  
APPLICANT: Hecht, Peter  
APPLICANT: Holtzman, Doug  
APPLICANT: Madden, Kevin  
APPLICANT: Maxon, Mary  
APPLICANT: Milne, Todd  
APPLICANT: No. US20020128250Alman, Thea  
APPLICANT: Royer, John  
APPLICANT: Salama, Sofie  
APPLICANT: Sherman, Amir  
APPLICANT: Silva, Jeff  
APPLICANT: Summers, Eric  
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
FILE REFERENCE: 109272.147  
CURRENT APPLICATION NUMBER: US/09/801.368  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 09/487,558  
PRIOR FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: US 60/160,587  
PRIOR FILING DATE: 1999-10-20  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 322  
LENGTH: 1536  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
US-09-801-368-322

Query Match 46.9%; Score 45; DB 3; Length 1536;  
Best Local Similarity 53.3%; Pred. No. 3.8e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGL 15  
Db 1370 IDGTEVDEEFSPEGI 1384

RESULT 10  
US-10-424-599-205669  
Sequence 205669, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 205669  
LENGTH: 89  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(89)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_27747C.1.pep  
US-10-424-599-205669

Query Match 45.8%; Score 44; DB 4; Length 89;  
Best Local Similarity 58.3%; Pred. No. 23;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GQKVDQFPQHG 14  
Db 46 GIKMDRMPQHG 57

RESULT 11  
US-10-450-763-36065  
Sequence 36065, Application US/10450763  
Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hysq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 36065  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(128)  
OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-36065

Query Match 45.8%; Score 44; DB 5; Length 128;  
Best Local Similarity 52.9%; Pred. No. 35;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DGQKVDQFPQHGLVKQ 18  
Db 60 DPQRPREQSPVHGLVQR 76

RESULT 12  
US-10-424-599-145103  
Sequence 145103, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 145103  
LENGTH: 130  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_102046C.1.pep  
US-10-424-599-145103

Query Match 45.8%; Score 44; DB 4; Length 130;  
Best Local Similarity 69.2%; Pred. No. 36;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKVDQFPQHGL 15  
Db 65 GQLQAEIIFPQHGL 77

RESULT 13  
US-10-450-763-36064  
Sequence 36064, Application US/10450763



; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 36064  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(159)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-36064

Query Match 45.8%; Score 44; DB 5; Length 159;  
Best Local Similarity 52.9%; Pred. No. 45;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DGQKVDQFPQHGVLVKQ 18  
Db 91 DPQRREQSPVHGLVQR 107

## RESULT 14

US-10-437-963-154933  
; Sequence 154933, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
Plants and Uses thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 154933

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_54746C.1.pep

US-10-437-963-154933

Query Match 45.8%; Score 44; DB 4; Length 387;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15  
Db 302 IEESFPQHGI 311

## RESULT 15

US-10-238-075-1472

; Sequence 1472, Application US/10238075

; Publication No. US20030148324A1  
; GENERAL INFORMATION:  
; APPLICANT: I.N.S.E.R.M.  
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolated  
; FILE REFERENCE: E.coli, and biological uses of these polynucleotides and of their  
; FILE REFERENCE: BLANDINE  
; CURRENT APPLICATION NUMBER: US/10/238,075  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 0003145  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1472  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-238-075-1472

Query Match 45.8%; Score 44; DB 4; Length 421;  
Best Local Similarity 43.8%; Pred. No. 1.3e+02;  
Matches 7; Conservative 7; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDEQFPQ--HGLVK 17  
Db 58 QKLEDEFPFTGLIR 73

Search completed: August 30, 2006, 05:12:59  
Job time : 91.9091 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 9.27273 Seconds  
(without alignments)  
133.695 Million cell updates/sec

Title: US-10-758-165a-11

Perfect score: 96

Sequence: 1 IDGQKVDQPPQHGLVKQ 18

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/US09\_NEW\_PUB.pdb:
- 2: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/US06\_NEW\_PUB.pdb:
- 3: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/US07\_NEW\_PUB.pdb:
- 4: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/US08\_NEW\_PUB.pdb:
- 5: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/PCT\_NEW\_PUB.pdb:
- 6: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/US10\_NEW\_PUB.pdb:
- 7: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/US11\_NEW\_PUB.pdb:
- 8: /EMC\_Celerra\_SID33/ptodata/1/pubpaa/US60\_NEW\_PUB.pdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	45.8	356	6	US-10-449-902-33028
2	44	45.8	376	6	US-10-449-902-47548
3	43	44.8	321	7	US-11-056-355B-6050
4	43	44.8	373	7	US-11-056-355B-6059
5	43	44.8	374	7	US-11-174-307B-286
6	43	44.8	400	7	US-11-174-307B-288
7	43	44.8	448	7	US-11-056-355B-6058
8	42	43.8	273	6	US-10-449-902-30777
9	42	43.8	314	7	US-11-056-355B-26554
10	42	43.8	314	7	US-11-056-355B-108652
11	42	43.8	314	7	US-11-056-355B-119891
12	42	43.8	328	6	US-10-953-349-26705
13	42	43.8	328	7	US-11-056-355B-26553
14	42	43.8	328	7	US-11-056-355B-68215
15	42	43.8	328	7	US-11-056-355B-108651
16	42	43.8	328	7	US-11-056-355B-119890
17	42	43.8	351	6	US-10-953-349-26704
18	42	43.8	351	7	US-11-056-355B-68214
19	42	43.8	353	7	US-11-330-403-2110
20	42	43.8	363	7	US-11-174-307B-2812
21	42	43.8	363	7	US-11-056-355B-26552
22	42	43.8	363	7	US-11-056-355B-108650
23	42	43.8	363	7	US-11-056-355B-119889
24	42	43.8	366	6	US-10-953-349-26703
25	42	43.8	366	7	US-11-056-355B-68213

26	41	42.7	286	7	US-11-056-355B-26724	Sequence 26724, A
27	41	42.7	286	7	US-11-056-355B-74037	Sequence 74037, A
28	41	42.7	477	7	US-11-330-403-7987	Sequence 7987, A
29	40	41.7	132	6	US-10-952-500-167	Sequence 167, App
30	40	41.7	292	7	US-11-330-403-11936	Sequence 11936, A
31	40	41.7	393	6	US-10-449-902-37067	Sequence 37067, A
32	40	41.7	415	7	US-11-056-355B-89336	Sequence 89336, A
33	40	41.7	415	7	US-11-056-355B-93092	Sequence 93092, A
34	40	41.7	455	7	US-11-056-355B-89335	Sequence 89335, A
35	40	41.7	455	7	US-11-056-355B-93091	Sequence 93091, A
36	40	41.7	469	7	US-11-056-355B-89334	Sequence 89334, A
37	40	41.7	469	7	US-11-056-355B-93090	Sequence 93090, A
38	39.5	41.1	576	7	US-11-330-403-4484	Sequence 4484, App
39	39	40.6	297	6	US-10-953-349-20831	Sequence 20831, A
40	39	40.6	299	6	US-10-953-349-20830	Sequence 20830, A
41	39	40.6	323	7	US-11-056-355B-30253	Sequence 30253, A
42	39	40.6	323	7	US-11-056-355B-30764	Sequence 30764, A
43	39	40.6	323	7	US-11-056-355B-33843	Sequence 33843, A
44	39	40.6	323	7	US-11-056-355B-34354	Sequence 34354, A
45	39	40.6	328	6	US-10-449-902-39837	Sequence 39837, A

#### ALIGNMENTS

##### RESULT 1

US-10-449-902-33028  
; Sequence 33028, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 33028  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-33028

Query Match 45.8%; Score 44; DB 6; Length 356;  
Best Local Similarity 60.0%; Pred. No. 12;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQPPQHGL 15  
Db 282 IEESPQHGI 291

##### RESULT 2

US-10-449-902-47548  
; Sequence 47548, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47548
; LENGTH: 376
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-47548

Query Match          45.8%; Score 44; DB 6; Length 376;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
Db      302 IEESFPQHGI 311

RESULT 3
US-11-056-355B-6060
; Sequence 6060, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 6060
; LENGTH: 321
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(321)
; OTHER INFORMATION: Ceres Seq. ID no. 12344159
US-11-056-355B-6060

Query Match          44.8%; Score 43; DB 7; Length 321;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
Db      246 VEEGFPQHGI 255

RESULT 4
US-11-056-355B-6059
; Sequence 6059, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 6059
; LENGTH: 373
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
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; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(373)
; OTHER INFORMATION: Ceres Seq. ID no. 12344158
US-11-056-355B-6059

Query Match          44.8%; Score 43; DB 7; Length 373;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
Db      298 VEEGFPQHGI 307

RESULT 5
US-11-174-307B-286
; Sequence 286, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174.307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 286
; LENGTH: 374
; TYPE: prt
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Transket_pyr; Pfam Description: Transketolase,
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Transketolase_C; Pfam Description: Transketolase,
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 520478; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3850999; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3851001; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3851003; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 25012844; NR Description: RH05604p [Drosophila
US-11-174-307B-286

Query Match          44.8%; Score 43; DB 7; Length 374;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
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RESULT 7  
US-11-056-355B-6058  
; Sequence 6058, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai

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RESULT 9
US-11-056-355B-26554
; Sequence 26554, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14

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; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 26554  
; LENGTH: 314  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(314)  
; OTHER INFORMATION: Ceres Seq. ID no. 12384700  
US-11-056-355B-26554

Query Match 43.8%; Score 42; DB 7; Length 314;  
Best Local Similarity 70.0%; Pred. No. 22;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15  
|:|||||:  
Db 246 VEEGFPQHG 255

## RESULT 10

US-11-056-355B-108652  
; Sequence 108652, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; PRIOR FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 108652  
; LENGTH: 314  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(314)  
; OTHER INFORMATION: Ceres Seq. ID no. 13668006  
US-11-056-355B-108652

Query Match 43.8%; Score 42; DB 7; Length 314;  
Best Local Similarity 70.0%; Pred. No. 22;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15  
|:|||||:  
Db 246 VEEGFPQHG 255

## RESULT 11

US-11-056-355B-119891  
; Sequence 119891, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 119891  
; LENGTH: 314

; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(314)  
; OTHER INFORMATION: Ceres Seq. ID no. 13668006  
US-11-056-355B-119891

Query Match 43.8%; Score 42; DB 7; Length 314;  
Best Local Similarity 70.0%; Pred. No. 22;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15  
|:|||||:  
Db 246 VEEGFPQHG 255

## RESULT 12

US-10-953-349-26705  
; Sequence 26705, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26705  
; LENGTH: 328  
; TYPE: PRP  
; ORGANISM: Triticum aestivum  
US-10-953-349-26705

Query Match 43.8%; Score 42; DB 6; Length 328;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15  
|:|||||:  
Db 260 VEEGFPQHG 269

## RESULT 13

US-11-056-355B-26553  
; Sequence 26553, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 26553  
; LENGTH: 328  
; TYPE: Prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(328)  
; OTHER INFORMATION: Ceres Seq. ID no. 12384699  
US-11-056-355B-26553

Query Match 43.8%; Score 42; DB 7; Length 328;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Search completed: August 30, 2006, 04:35:56  
Job time : 9.27273 secs

Qy 6 VDEQFPQHGL 15  
|:|:|:|:|:  
Db 260 VEGFPQHG 269

## RESULT 14

US-11-056-355B-68215  
; Sequence 68215, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 68215  
; LENGTH: 328  
; TYPE: prt  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(328)  
; OTHER INFORMATION: Ceres Seq. ID no. 13596007  
US-11-056-355B-68215

Query Match 43.8%; Score 42; DB 7; Length 328;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15  
|:|:|:|:|:  
Db 260 VEGFPQHG 269

## RESULT 15

US-11-056-355B-108651  
; Sequence 108651, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 108651  
; LENGTH: 328  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(328)  
; OTHER INFORMATION: Ceres Seq. ID no. 13668005  
US-11-056-355B-108651

Query Match 43.8%; Score 42; DB 7; Length 328;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15  
|:|:|:~|:|:  
Db 260 VEGFPQHG 269

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